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Scientific and Technical Information Center

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If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Other (specify) _____

PTO-1590 (8-01)

; Entered [jdelaval 10-Jun-02 5:57]
09-251073
eildv1

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:28:11 ; Search time 14.16 Seconds
(without alignments)
33.930 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: June 10, 2002, 06:28:47
Job time: 36 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:29:26 ; Search time 11.79 Seconds
(without alignments)
16.421 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: June 10, 2002, 06:33:29
Job time: 243 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:28:11 ; Search time 24.93 Seconds
(without alignments)
34.696 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: June 10, 2002, 06:30:53
Job time: 162 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:28:11 ; Search time 15.32 Seconds
(without alignments)
25.031 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 233302 seqs, 76696041 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: June 10, 2002, 06:31:29
Job time: 198 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:28:11 ; Search time 24.35 Seconds
(without alignments)
22.808 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	100.0	5	17	AAR95719	Alpha-4Beta-1 inte
2	23	100.0	5	18	AAW25192	LDV-peptide capabl
3	23	100.0	5	19	AAW46318	Peptide recognised
4	23	100.0	5	20	AAY03855	Integrin ligand di
5	23	100.0	5	21	AAY80488	Cell adhesion pept
6	23	100.0	5	21	AAY77442	Fibronectin CS1-de
7	23	100.0	5	21	AAY69619	VLA-4 inhibitor pe
8	23	100.0	5	22	AAB73465	Fibronectin VLA-4
9	23	100.0	5	22	AAB91966	Fibronectin fragme
10	23	100.0	5	22	AAB50876	Integrin recogniti
11	23	100.0	5	22	AAB59135	Peptide #3 recogni

ALIGNMENTS

RESULT 1
AAR95719
ID AAR95719 standard; peptide; 5 AA.
XX
AC AAR95719;
XX
DT 04-DEC-1996 (first entry)
XX
DE Alpha-4Beta-1 integrin binding inhibitory peptide 16.
XX
KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW inhibitor; binding; white blood cell; migration; capillary wall;
KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW CS1; CS5; H1; LDV; active site.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 5
FT /note= "Val-NH2"
XX
PN US5510332-A.
XX
PD 23-APR-1996.
XX
PF 07-JUL-1994; 94US-0271830.
XX
PR 07-JUL-1994; 94US-0271830.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Beck PJ, Kogan TP, Ren K, Vanderslice P;
XX
DR WPI; 1996-221274/22.
XX
PT New peptide(s) based on the LDV domain of fibronectin - used for
PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT fibronectin or invasin
XX
PS Disclosure; Column 21-22; 35pp; English.
XX
CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
CC surface of endothelial cells that line the interior wall of capillaries.
CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
CC white blood cells to adhere to the capillary wall in areas where the
CC tissue surrounding the capillary has been infected or damaged. Sometimes
CC this white blood cell migration can become uncontrolled, with white
CC blood cells flooding to the scene, causing widespread tissue damage.
CC Cpds. capable of blocking this process may be beneficial as therapeutic
CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC fibronectin. Three distinct IA4B1-binding sites have been identified
CC within fibronectin. One site is found in the HeplI region and is
CC expressed in all isoforms; two others (CS1 and CS5) are present in the
CC alternatively spliced type III connecting segments. CS1 has the higher
CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC peptide that include the LDV domain presented in such a way by its novel
CC flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   2
AAW25192
ID   AAW25192 standard; peptide; 5 AA.
XX
AC   AAW25192;
XX
DT   05-JAN-1998  (first entry)
XX
DE   LDV-peptide capable of binding cell adhesion molecules.
XX
KW   LDV; leucine; aspartic acid; valine; cell adhesion molecule;
KW   binding; bladder irrigation; tumour removal; endoscopic operation;
KW   transurethral resection; cancer; neoplasia.
XX
OS   Synthetic.
XX
PN   DE19529909-A1.
XX
PD   20-FEB-1997.
XX
PF   15-AUG-1995;   95DE-1029909.
XX
PR   15-AUG-1995;   95DE-1029909.
XX
PA   (FREP ) FRESENIUS AG.
XX
PI   Boehle A;
XX
DR   WPI; 1997-133793/13.
XX
PT   Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
PT   adhesion molecules
XX
PS   Claim 6; Page 8; 8pp; German.
XX
CC   AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
CC   The peptides are capable of binding to cell adhesion molecules and
CC   are used in aqueous irrigation solutions for use during and after
CC   endoscopic operations. Preferred irrigation solutions are
CC   electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
CC   oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
CC   GPRP, VTL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid
CC   code). The solutions are especially used for irrigating the bladder
CC   during and after tumour removal by transurethral resection. The
CC   peptides protect against recurrence of tumours.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 23;  DB 18;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   3
AAW46318
ID   AAW46318 standard; Protein; 5 AA.
XX
AC   AAW46318;
XX
DT   08-MAY-1998  (first entry)
XX
DE   Peptide recognised by integrin alpha4eta1.
XX
KW   Fibrinogen; integrin; alpha-IIb-beta3; cell surface receptor;
KW   penton base protein; coat proteins; adenovirus; binding site;
KW   cellular adhesion; extracellular matrix molecule; binding domain;
KW   cell surface binding site; bispecific molecule; gene therapy.
XX
OS   Unidentified.
XX
PN   US5712136-A.
XX
PD   27-JAN-1998.
XX
PF   17-APR-1996;   96US-0634060.
XX
PR   08-SEP-1994;   94US-0303162.
XX
PA   (GENV-) GENVEC INC.
XX
PI   Brough DE,  Bruder JT,  Kovesdi I,  McVey DL,  Roelvink PW;
PI   Wickham TJ;
XX
DR   WPI; 1998-119984/11.
XX
PT   Methods for introducing adenovirus into cells - used for genetic
PT   engineering and gene therapy
XX
PS   Claim 27; Column 2; 56pp; English.
XX
CC   The present sequence is a linear stretch of amino acids (present in
CC   fibronectin) recognised by the integrin alpha4beta1. Integrins are
CC   cell surface receptors. The penton base protein (one of the coat
CC   proteins) of adenoviruses binds to integrins. The integrins not only
CC   provide a binding site for the adenoviral penton base protein, but also
CC   mediate cellular adhesion to the extracellular matrix molecules. The
CC   specification describes a method of introducing an adenovirus into
CC   a cell in vitro having a particular cell surface binding site. The
CC   adenovirus is contacted with a bispecific molecule comprising a component
CC   that selectively binds a binding domain of the penton base protein of the
CC   adenovirus and a second component that selectively binds the cell surface
CC   binding site. A complex of the adenovirus and the bispecific molecule is
CC   formed, and the  cell is contacted with it to allow entry of the
CC   adenovirus into the cell. The methods can be used for research and the
CC   vectors can be used for gene therapy.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 23;  DB 19;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   4
AAY03855
ID   AAY03855 standard; peptide; 5 AA.
XX
AC   AAY03855;
XX
DT   16-JUN-1999  (first entry)
XX
DE   Integrin ligand dissociator (ILD) peptide.
XX
KW   Integrin-ligand; dissociator; disaggregation; platelet thrombus; stroke;
KW   fibrinogen; glycoprotein IIb-IIIa; angina; myocardial infarction; bone;
KW   osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy;
KW   psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
KW   organ transplant rejection; arthritis; ILD.
XX
OS   Synthetic.
XX
```

PN WO9911280-A1.
XX
PD 11-MAR-1999.
XX
PF 03-SEP-1998; 98WO-US18305.
XX
PR 03-SEP-1997; 97US-0057463.
XX
PA (BURN-) BURNHAM INST.
XX
PI Hu DD, Smith JW;
XX
DR WPI; 1999-243586/20.
XX
PT Disaggregating a ligand:integrin receptor complex
XX
PS Disclosure; Page 10; 39pp; English.
XX
CC The invention relates to integrin ligand dissociators. Disaggregation of
CC an existing platelet thrombus in a blood vessel is due to dissociation of
CC fibrinogen from glycoprotein IIb-IIIa. This dissociation is caused by the
CC binding of an integrin-ligand dissociator at ligand binding site I of
CC glycoprotein IIb-IIIa. The invention provides a method of disaggregating
CC an existing platelet thrombus in a blood vessel, where the platelet
CC thrombus may form an occlusion of a blood vessel, in a subject comprises
CC administering a compound which dissociates fibrinogen bound to a first
CC site on platelet glycoprotein IIb-IIIa, by binding to a second
CC interacting site on platelet glycoprotein IIb-IIIa, disaggregating the
CC platelet thrombus. The method is used to treat humans with unstable
CC angina, stroke and/or acute myocardial infarction. The methods can be
CC used to enact de-adhesion of osteoclasts from the bone surface to halt
CC bone loss in a patient with osteoporosis. The methods can also be used
CC for the de-adhesion of angiogenic endothelial cells in a patient with a
CC pathologic condition associated with angiogenesis, e.g. cancer, diabetic
CC retinopathy, psoriasis. The methods can also be used to treat tumours,
CC atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory
CC bowel disease, or organ transplant rejection, and asthma. The methods can
CC be used for the dissolution of pre-formed platelet aggregates, which is a
CC departure from the current strategy of treatment prior to formation of
CC vascular occlusions. The present sequence represents an integrin ligand
CC dissociator (ILD) that can be used in the method of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 5
AAY80488
ID AAY80488 standard; peptide; 5 AA.
XX
AC AAY80488;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cell adhesion peptide #23.
XX
KW Bone regenerative; osteopathic; osseous tissue; reconstitution;
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.
XX
OS Synthetic.
XX
PN WO200004941-A1.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16800.
XX
PR 24-JUL-1998; 98US-0122348.
XX
PA (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
XX
PI Budny JA;
XX
DR WPI; 2000-195084/17.
XX
PT System for reconstructing osseous tissue, useful e.g. for treating
PT fractures, comprises scaffold containing promoter of bone formation and
PT inhibitor of bone resorption -
XX
PS Claim 14; Page 32; 44pp; English.
XX
CC The invention relates to a novel system for reconstitution of osseous
CC tissue comprising a scaffold carrying a compound (I) that promotes
CC bone formation and a component that decreases bone resorption (II).
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular
CC matrix. (I) is preferably selected from: selectin or selectin binding
CC fragments, proteins and peptides that facilitate cell adhesion,
CC plasminogen activator inhibitors, protease inhibitors and
CC metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed
CC examples of cell adhesion peptides used in the system of the invention.
CC The system is used to replace, remodel or correct bone defects, e.g.
CC fractures, fissures or bone mass loss. Incorporation of (I) into the
CC scaffold results in rapid seeding by osteoblasts and the development of
CC an organic matrix, i.e. the preformed scaffold replaces the
CC rate-determining step of extracellular matrix formation. The scaffold can
CC be designed to have a predetermined resorption/degradation rate, and may
CC include regulatory compounds for specific cell types.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 6
AAY77442
ID AAY77442 standard; peptide; 5 AA.
XX
AC AAY77442;
XX
DT 22-MAY-2000 (first entry)
XX
DE Fibronectin CS1-derived peptide #33.
XX
KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS Mammalia.
XX
PN WO200002903-A1.
XX
PD 20-JAN-2000.
XX
PF 15-DEC-1998; 98WO-US26605.
XX
PR 10-JUL-1998; 98US-0113689.
XX
PA (CYTE-) CYTEL CORP.
XX

PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX
DR WPI; 2000-182213/16.
XX
PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders -
XX
PS Disclosure; Fig 2; 243pp; English.
XX
CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAY77410).
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 7
AAY69619
ID AAY69619 standard; peptide; 5 AA.
XX
AC AAY69619;
XX
DT 19-APR-2000 (first entry)
XX
DE VLA-4 inhibitor peptide #2.
XX
KW LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1;
KW CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative;
KW arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder;
KW autoimmune disorder; respiratory disorder; LDV motif.
XX
OS Synthetic.
XX
PN WO200000477-A1.
XX
PD 06-JAN-2000.
XX
PF 31-MAY-1999; 99WO-IB00973.
XX
PR 30-JUN-1998; 98US-0091180.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Duplantier AJ, Milici AJ, Chupak LS;
XX
DR WPI; 2000-126762/11.
XX
PT Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives -
XX
PS Disclosure; Page 2; 120pp; English.
XX
CC The invention relates to novel arylalkyl and arylureidoalkyl
CC azolylalkanoic acid derivatives and related compounds (I), and their
CC salts and prodrugs. These are are integrin inhibitors, specifically of
CC VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29),
CC which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
CC inducible cell surface protein VCAM-1 (vascular cell adhesion
CC molecule-1) and for the alternatively spliced forms of fibronectin (FN)
CC which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
CC and consequent or associated pathogenic processes mediated by VLA-4, and
CC may therefore be useful in the treatment and prevention of inflammatory,
CC autoimmune, or respiratory disorders . These include asthma, arthritis,
CC psoriasis, multiple sclerosis, transplant rejection, diabetes, and
CC inflammatory bowel disease. Sequences AAY69618-Y69620 represent peptides
CC derived from the VLA-4-binding domain of the FN CS-1 region which
CC contain the LDV motif and are known to inhibit fibronectin-dependent
CC cell adhesion.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 8
AAB73465
ID AAB73465 standard; peptide; 5 AA.
XX
AC AAB73465;
XX
DT 02-JUL-2001 (first entry)
XX
DE Fibronectin VLA-4 binding domain-derived pentapeptide #1.
XX
KW Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
KW very late antigen; antibody; kidney disease; chronic renal failure;
KW end-stage renal disease; chronic diabetic nephropathy;
KW diabetic glomerulopathy; diabetic renal hypertrophy;
KW hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
KW chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
KW nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
XX
OS Unidentified.
XX
PN WO200119396-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US25140.
XX
PR 14-SEP-1999; 99US-0153826.
XX
PA (BIOJ) BIOGEN INC.
PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
XX
PI Allen A, Pusey C, Lobb R;
XX
DR WPI; 2001-273408/28.
XX

PT Treating a mammal in, or at a risk of developing, chronic renal
PT failure, involves administering at least one integrin antagonist to the
PT mammal -
XX
PS Disclosure; Page 24; 62pp; English.
XX
CC The invention relates to a method for treating a mammal with,
CC or at risk of developing, chronic renal failure, involving the
CC administration of at least one integrin antagonist. The integrin
CC antagonists that may be used in the method include antagonists of
CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
CC containing integrins. In particular, the antagonists are antibodies
CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in
CC the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).
CC The method of the invention may be used to treat chronic renal failure,
CC end-stage renal disease, chronic diabetic nephropathy, diabetic
CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
CC hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary
CC nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
CC peptides derived from the VLA-4 binding domain (CS-1 region) of
CC fibronectin, which inhibit fibronectin-dependent cell adhesion, and may
CC therefore be used in the method of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 9
AAB91966
ID AAB91966 standard; Peptide; 5 AA.
XX
AC AAB91966;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1142.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 569; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 10
AAB50876
ID AAB50876 standard; peptide; 5 AA.
XX
AC AAB50876;
XX
DT 19-MAR-2001 (first entry)
XX
DE Integrin recognition peptide sequence #3.
XX
KW Integrin; transmembrane protein; alpha4 integrin inhibitor;
KW paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
KW multiple sclerosis; asthma; atherosclerosis; wound healing.
XX
OS Unidentified.
XX
PN WO200073342-A1.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15153.
XX
PR 01-JUN-1999; 99US-0323447.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ginsberg MH, Pfaff M, Liu S;
XX
DR WPI; 2001-070959/08.
XX
PT Polypeptides useful in construction of structural models for
PT identifying therapeutic compounds, comprises series of heptad repeats
PT that mimic a transmembrane domain and cytoplasmic domain attached to
PT heptad repeats -
XX
PS Disclosure; Page 2; 37pp; English.
XX
CC The present sequence is given in a specification relating to a
CC polypeptide comprising a series of heptad-repeats that mimic a
CC transmembrane domain, and a selected cytoplasmic domain attached to the

CC heptad repeats. At least a portion of the polypeptide is prepared
CC recombinantly or at least 1 heptad repeat in the series has a different
CC amino acid sequence to other heptad repeats in the series. The
CC polypeptide is useful in the construction of structural models which are
CC useful for evaluating structure and activity of a selected occupied and
CC clustered transmembrane protein having the selected cytoplasmic domain
CC and for identifying therapeutic compounds. It is also useful for
CC identifying agents as inhibitors of alpha4 integrin biological
CC responses by contacting the structural model with paxillin or a
CC paxillin related molecule in the presence and absence of a test agent
CC and determining binding of paxillin or paxillin related molecule to the
CC structural model. A decrease in binding in the presence of the test
CC agent indicates that the test agent is an inhibitor of alpha4 integrin
CC biological response. Inhibitors of the binding of paxillin to alpha4 are
CC useful in blocking immune responses in conditions such as inflammatory
CC bowel disease, arthritis, multiple sclerosis and asthma and in
CC inhibiting atherosclerosis and scarring during wound healing.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 11
AAB59135
ID AAB59135 standard; peptide; 5 AA.
XX
AC AAB59135;
XX
DT 21-MAR-2001 (first entry)
XX
DE Peptide #3 recognised by integrin.
XX
KW Heptad repeat; transmembrane domain; cytoplasmic; integrin;
KW inflammation; thrombosis; malignancy.
XX
OS Synthetic.
XX
PN WO200073341-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14656.
XX
PR 27-MAY-1999; 99US-0320907.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ginsberg MH, Pfaff M;
XX
DR WPI; 2001-041143/05.
XX
PT Polypeptides useful in construction of structural models for
PT identifying therapeutic compounds, comprises series of heptad repeats
PT that mimic a transmembrane domain and cytoplasmic domain attached to
PT the repeats -
XX
PS Disclosure; Page 2; 36pp; English.
XX
CC The present invention relates to a peptide with a series of
CC heptad-repeats that mimic a transmembrane domain and a selected
CC cytoplasmic domain attached to the heptad repeats. The invention
CC is useful for evaluating structure and activity of a selected
CC occupied and clustered transmembrane protein with the selected
CC cytoplasmic domain and for identifying therapeutic compounds. It
CC is also useful for identifying a cytoplasmic domain binding partner.
CC It is may be used to study protein interactions with transmembrane
CC proteins such as integrin, which can be used to treat conditions in
CC which over activity of integrins is involved, such as inflammation,
CC thrombosis and malignancy.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

Search completed: June 10, 2002, 06:30:08
Job time: 117 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:17:45 ; Search time 14.7 Seconds
(without alignments)
32.683 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	100.0	50	2	B86576	hypothetical prote
2	23	100.0	50	2	C72047	hypothetical prote
3	23	100.0	107	2	S13787	conserved hypothet
4	23	100.0	119	1	A69441	conserved hypothet
5	23	100.0	119	2	F84272	hypothetical prote
6	23	100.0	143	2	C44259	kinesin heavy chai
7	23	100.0	146	2	E90645	probable PTS enzym
8	23	100.0	146	2	E85496	probable PTS enzym
9	23	100.0	147	2	F70814	hypothetical prote
10	23	100.0	147	2	AG0772	probable exported
11	23	100.0	156	2	G82906	transcription elon
12	23	100.0	169	2	AH0568	phosphoribosylamin
13	23	100.0	172	2	S24397	stellate protein -
14	23	100.0	172	2	S24398	stellate protein -
15	23	100.0	174	2	AF0390	shikimate kinase (
16	23	100.0	174	2	F97114	uncharacterized co
17	23	100.0	177	2	A64431	hypothetical prote
18	23	100.0	180	2	G95148	conserved hypothet
19	23	100.0	180	2	E98016	conserved hypothet
20	23	100.0	200	2	T48130	hypothetical prote
21	23	100.0	217	1	ZZZRBM	nodulation protein
22	23	100.0	217	1	ZZZRB4	nodulation protein
23	23	100.0	217	2	B95321	NodB chitooligosac
24	23	100.0	222	2	C72400	conserved hypothet
25	23	100.0	231	2	B98297	hypothetical prote
26	23	100.0	231	2	AE2986	conserved hypothet
27	23	100.0	242	2	A69026	conserved hypothet
28	23	100.0	250	2	B91020	hypothetical prote
29	23	100.0	250	2	D85864	hypothetical prote
30	23	100.0	253	2	H70188	conserved hypothet
31	23	100.0	256	2	T32649	hypothetical prote
32	23	100.0	261	2	C55581	nasD protein - Kle
33	23	100.0	266	2	A95300	Nitrate transport
34	23	100.0	267	2	H90388	erythrocyte band 7
35	23	100.0	267	2	C64995	hypothetical prote
36	23	100.0	271	2	C86907	regulator of purin
37	23	100.0	286	2	S01402	H+-transporting AT
38	23	100.0	289	2	E97820	3-demethylubiquino
39	23	100.0	290	2	T21185	hypothetical prote
40	23	100.0	307	2	G81905	probable sulfate a
41	23	100.0	307	2	B81111	sulfate adenylyltr
42	23	100.0	307	2	S20383	phytoene synthase
43	23	100.0	312	2	T41157	probable 60s acidi
44	23	100.0	320	2	S73413	transcription anti
45	23	100.0	321	2	A95182	hypothetical prote

ALIGNMENTS

RESULT 1
B86576
hypothetical protein CPj0685 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: B86576
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Accession: B86576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <STO>
A;Cross-references: GB:BA000008; NID:g8979057; PIDN:BAA98892.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0685

Query Match 100.0%; Score 23; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 eildv 5
          |||||
Db      7 EILDV 11
```

RESULT 2
C72047
hypothetical protein - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: C72047
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Accession: C72047
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <ARN>
A;Cross-references: GB:AE001651; GB:AE001363; NID:g4376985; PIDN:AAD18824.1; PID:g437
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: CPn0685

Query Match 100.0%; Score 23; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 eildv 5
          |||||
Db      7 EILDV 11


RESULT   3
S13787
conserved hypothetical protein yaaK - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: S13787; S66050; C69737
R;Alonso, J.C.; Shirahige, K.; Ogasawara, N.
Nucleic Acids Res. 18, 6771-6777, 1990
A;Title: Molecular cloning, genetic characterization and DNA sequence analysis of the re
A;Reference number: S13786; MUID:91088245
A;Accession: S13787
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <ALO>
A;Cross-references: EMBL:X17014; NID:g453238; PIDN:CAA34878.1; PID:g40073
R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
DNA Res. 1, 1-14, 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom
A;Reference number: S65967; MUID:96051385
A;Accession: S66050
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <OGA>
A;Cross-references: EMBL:D26185; NID:g467326; PIDN:BAA05256.1; PID:g467410
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033
A;Accession: C69737
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-107 <KUN>
A;Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11796.1; PID:g2632287
A;Experimental source: strain 168
C;Genetics:
A;Gene: yaaK
C;Superfamily: Escherichia coli ybaB protein


  Query Match             100.0%;  Score 23;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     52 EILDV 56


RESULT   4
A69441
conserved hypothetical protein AF1530 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A69441
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Reference number: A69250; MUID:98049343
A;Accession: A69441
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-119 <KLE>
A;Cross-references: GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AAB89718.1; PID:g264
C;Superfamily: conserved hypothetical protein MJ0039


  Query Match             100.0%;  Score 23;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    109 EILDV 113


RESULT   5
F84272
hypothetical protein Vng1169c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: F84272
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
 Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483
A;Accession: F84272
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <STO>
A;Cross-references: GB:AE004437; NID:g10580704; PIDN:AAG19546.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1169C
C;Superfamily: conserved hypothetical protein MJ0039


  Query Match             100.0%;  Score 23;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    110 EILDV 114


RESULT   6
C44259
kinesin heavy chain homolog KIF5 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998
C;Accession: C44259
R;Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous system.
A;Reference number: A44259; MUID:93077686
A;Accession: C44259
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-143 <AIZ>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118906)
C;Superfamily: kinesin heavy chain; kinesin motor domain homology
```

F;1-143/Domain: kinesin motor domain homology (fragment) <KMOT>

Query Match 100.0%; Score 23; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 91 EILDV 95

RESULT 7
E90645
probable PTS enzyme II B component [imported] - Escherichia coli (strain O157:H7, substr
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: E90645
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90645
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33556.1; PID:g13359589; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0133

Query Match 100.0%; Score 23; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 15 EILDV 19

RESULT 8
E85496
probable PTS enzyme II B component [imported] - Escherichia coli (strain O157:H7, substr
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E85496
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <STO>
A;Cross-references: GB:AE005174; NID:g12512844; PIDN:AAG54433.1; GSPDB:GN00145; UWGP:Z01
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yadI

Query Match 100.0%; Score 23; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 15 EILDV 19

RESULT 9
F70814
hypothetical protein Rv0854 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: F70814
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A;Reference number: A70500; MUID:98295987
A;Accession: F70814
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-147 <COL>
A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA17660.1; PID:g291
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0854
C;Superfamily: Streptomyces coelicolor hypothetical protein SC6G10.02c

Query Match 100.0%; Score 23; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 17 EILDV 21

RESULT 10
AG0772
probable exported protein STY2351 [imported] - Salmonella enterica subsp. enterica se
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0772
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0772
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02501.1; PID:g16503365; GSPDB:GN00176
C;Genetics:
A;Gene: STY2351

Query Match 100.0%; Score 23; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 98 EILDV 102

RESULT 11
G82906
transcription elongation factor UU304 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: G82906
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a

A;Reference number: A82870
A;Accession: G82906
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <GLA>
A;Cross-references: GB:AE002128; GB:AF222894; NID:g6899279; PIDN:AAF30713.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: greA; UU304
A;Genetic code: SGC3
C;Superfamily: transcription elongation factor greb
C;Keywords: transcription factor

Query Match 100.0%; Score 23; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 20 EILDV 24

RESULT 12
AH0568
phosphoribosylaminoimidazole carboxylase catalytic chain [imported] - Salmonella enteric
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH0568
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AH0568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05018.1; PID:g16501801; GSPDB:GN00176
C;Genetics:
A;Gene: STY0582
C;Superfamily: phosphoribosylaminoimidazole carboxylase catalytic chain; phosphoribosyla

Query Match 100.0%; Score 23; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 31 EILDV 35

RESULT 13
S24397
stellate protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Feb-1994 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C;Accession: S24397; S08120
R;Livak, K.J.
Genetics 124, 303-316, 1990
A;Title: Detailed structure of the Drosophila melanogaster Stellate genes and their tran
A;Reference number: S24397; MUID:90169476
A;Accession: S24397
A;Molecule type: DNA
A;Residues: 1-172 <LIV>
A;Cross-references: EMBL:X15899; NID:g8660; PIDN:CAA33906.1; PID:g295755
C;Genetics;
A;Gene: stellate
A;Cross-references: FlyBase:FBgn0003523
A;Introns: 4/2; 171/2

Query Match 100.0%; Score 23; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 46 EILDV 50

RESULT 14
S24398
stellate protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S24398
R;Livak, K.J.
Genetics 124, 303-316, 1990
A;Title: Detailed structure of the Drosophila melanogaster Stellate genes and their t
A;Reference number: S24397; MUID:90169476
A;Accession: S24398
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-172 <LIV>

Query Match 100.0%; Score 23; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 46 EILDV 50

RESULT 15
AF0390
shikimate kinase (EC 2.7.1.71) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 11-Jan-2002
C;Accession: AF0390
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92450.1; PID:g15981151; GSPDB:GN00175
C;Genetics:
A;Gene: aroL
C;Superfamily: shikimate kinase; shikimate kinase homology
C;Keywords: phosphotransferase

Query Match 100.0%; Score 23; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 131 EILDV 135

Search completed: June 10, 2002, 06:23:16
Job time: 331 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:20:35 ; Search time 11.71 Seconds
(without alignments)
16.533 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	100.0	107	1	YAAK_BACSU	P24281 bacillus su
2	23	100.0	121	1	PAND_WOLSU	O34246 wolinella s
3	23	100.0	156	1	GREA_UREPA	Q9pqi7 ureaplasma
4	23	100.0	172	1	STEL_DROME	P15021 drosophila
5	23	100.0	177	1	YA50_METJA	Q58450 methanococc
6	23	100.0	198	1	IFE2_ARATH	O04663 arabidopsis
7	23	100.0	217	1	NODB_RHIME	P02963 rhizobium m
8	23	100.0	229	1	ACHP_LYMST	P58154 lymnaea sta
9	23	100.0	259	1	DJBA_MOUSE	Q9qyi5 mus musculu
10	23	100.0	262	1	NASD_KLEPN	P39459 klebsiella
11	23	100.0	267	1	YFAU_ECOLI	P76469 escherichia
12	23	100.0	271	1	PURR_LACLA	O53065 lactococcus
13	23	100.0	286	1	ATPG_BACP3	P09222 bacillus ps
14	23	100.0	287	1	ATPG_BACCA	P41010 bacillus ca
15	23	100.0	287	1	ATPG_BACST	P42007 bacillus st
16	23	100.0	307	1	CRTB_SYNP7	P37269 synechococc
17	23	100.0	320	1	Y054_MYCPN	P75049 mycoplasma
18	23	100.0	332	1	SD22_SCHPO	P22194 schizosacch
19	23	100.0	338	1	DHAS_SHESP	Q56732 shewanella
20	23	100.0	338	1	DHAS_SHEVI	Q56734 shewanella
21	23	100.0	342	1	LYC_CLOPE	P26836 clostridium
22	23	100.0	344	1	FLIG_BORBU	P52610 borrelia bu
23	23	100.0	351	1	DJB2_HUMAN	P25686 homo sapien
24	23	100.0	366	1	DP3B_ECOLI	P00583 escherichia
25	23	100.0	366	1	DP3B_SALTY	P26464 salmonella
26	23	100.0	380	1	P37_MYCPN	P75371 mycoplasma
27	23	100.0	380	1	RPA2_ARCFU	O28390 archaeoglob
28	23	100.0	380	1	YXEP_BACSU	P54955 bacillus su
29	23	100.0	387	1	2A5E_MOUSE	Q61151 m serine/th
30	23	100.0	394	1	CEGT_HUMAN	Q16739 homo sapien
31	23	100.0	414	1	YAFA_ECOLI	P04335 escherichia
32	23	100.0	414	1	YAFA_SALTY	P37722 salmonella
33	23	100.0	435	1	2A5G_MOUSE	Q60996 m serine/th
34	23	100.0	467	1	2A5E_HUMAN	Q16537 h serine/th
35	23	100.0	472	1	YA65_MOUSE	P46938 mus musculu
36	23	100.0	484	1	DCOR_NEUCR	P27121 neurospora
37	23	100.0	486	1	2A5A_HUMAN	Q15172 h serine/th
38	23	100.0	493	1	PYR5_DROME	Q01637 drosophila
39	23	100.0	497	1	2A5B_HUMAN	Q15173 homo sapien
40	23	100.0	500	1	2A5B_RABIT	Q28647 o serine/th
41	23	100.0	503	1	GLPK_PSETO	O87924 pseudomonas
42	23	100.0	506	1	SYG_DEIRA	Q9rsr5 deinococcus
43	23	100.0	522	1	FINC_CANFA	Q28275 canis famil
44	23	100.0	522	1	FINC_HORSE	Q28377 equus cabal
45	23	100.0	524	1	2A5G_HUMAN	Q13362 h serine/th

ALIGNMENTS

RESULT 1
YAAK_BACSU
ID YAAK_BACSU STANDARD; PRT; 107 AA.
AC P24281;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yaaK.
GN YAAK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088245; PubMed=2124672;
RA Alonso C., Shirahige K., Ogasawara N.;
RT "Molecular cloning, genetic characterization and DNA sequence
RT analysis of the recM region of Bacillus subtilis.";
RL Nucleic Acids Res. 18:6771-6777(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
CC -!- SIMILARITY: BELONGS TO THE UPF0133 FAMILY.
CC ---

CC ---
DR EMBL; X17014; CAA34878.1; -.
DR EMBL; D26185; BAA05256.1; -.
DR EMBL; Z99104; CAB11796.1; -.
DR PIR; S13787; S13787.
DR SubtiList; BG10084; yaaK.
DR InterPro; IPR003727; DUF149.
DR Pfam; PF02575; DUF149; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 107 AA; 11781 MW; DB3EBA3420F6A9E6 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 52 EILDV 56

```
RESULT   2
PAND_WOLSU
ID   PAND_WOLSU     STANDARD;      PRT;   121 AA.
AC   O34246;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Aspartate 1-decarboxylase precursor (EC 4.1.1.11) (Aspartate alpha-
DE   decarboxylase).
GN   PAND.
OS   Wolinella succinogenes.
OC   Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC   Wolinella.
OX   NCBI_TaxID=844;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gross R., Simon J., Theis F., Kroeger A.;
RT   "Two membrane anchors of Wolinella succinogenes hydrogenase and their
RT   function in fumarate and polysulfide respiration.";
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: L-aspartate = beta-alanine + CO(2).
CC   -!- COFACTOR: Pyruvoyl group (By similarity).
CC   -!- PATHWAY: Pantothenate biosynthesis; second branch.
CC   -!- SIMILARITY: BELONGS TO THE PAND FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ003049; CAA05822.1; -.
DR   HSSP; P31664; 1AW8.
DR   InterPro; IPR003190; Asp_decarbox.
DR   Pfam; PF02261; Asp_decarbox; 1.
KW   Pantothenate biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen.
FT   CHAIN         1     24       ASPARTATE 1-DECARBOXYLASE BETA CHAIN (BY
FT                                SIMILARITY).
FT   CHAIN        25    121       ASPARTATE 1-DECARBOXYLASE ALPHA CHAIN (BY
FT                                SIMILARITY).
FT   MOD_RES      25     25       CONVERTED TO A PYRUVOYL GROUP (BY
FT                                SIMILARITY).
SQ   SEQUENCE   121 AA;  13601 MW;  41FB7B63B571F837 CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     45 EILDV 49


RESULT   3
GREA_UREPA
ID   GREA_UREPA     STANDARD;      PRT;   156 AA.
AC   Q9PQI7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transcription elongation factor greA (Transcript cleavage factor
DE   greA).
GN   GREA OR UU304.
OS   Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC   Mycoplasmataceae; Ureaplasma.
OX   NCBI_TaxID=134821;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROVAR 3;
RX   MEDLINE=20500219; PubMed=11048724;
RA   Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA   Cassell G.H.;
RT   "The complete sequence of the mucosal pathogen Ureaplasma
RT   urealyticum.";
RL   Nature 407:757-762(2000).
CC   -!- FUNCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION
CC       ELONGATION PAST TEMPLATE-ENCODED ARRESTING SITES. THE ARRESTING
CC       SITES IN DNA HAVE THE PROPERTY OF TRAPPING A CERTAIN FRACTION
CC       OF ELONGATING RNA POLYMERASES THAT PASS THROUGH, RESULTING IN
CC       LOCKED TERNARY COMPLEXES. CLEAVAGE OF THE NASCENT TRANSCRIPT BY
CC       CLEAVAGE FACTORS SUCH AS GREA OR GREB ALLOWS THE RESUMPTION OF
CC       ELONGATION FROM THE NEW 3'TERMINUS. GREA RELEASES SEQUENCES OF
CC       2 TO 3 NUCLEOTIDES (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE GREA/GREB FAMILY.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE002128; AAF30713.1; -.
DR   InterPro; IPR001437; GreA_GreB.
DR   Pfam; PF01272; GreA_GreB; 1.
DR   ProDom; PD004918; GreA_GreB; 1.
DR   PROSITE; PS00829; GREAB_1; 1.
DR   PROSITE; PS00830; GREAB_2; FALSE_NEG.
KW   Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
FT   DOMAIN        7     24       COILED COIL (POTENTIAL).
FT   DOMAIN       42     84       COILED COIL (POTENTIAL).
SQ   SEQUENCE   156 AA;  17767 MW;  86BEA8EC07C96461 CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     20 EILDV 24


RESULT   4
STEL_DROME
ID   STEL_DROME     STANDARD;      PRT;   172 AA.
AC   P15021;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Stellate protein.
GN   STE.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OREGON-R; TISSUE=Testis;
RX   MEDLINE=90169476; PubMed=1689686;
RA   Livak K.J.;
RT   "Detailed structure of the Drosophila melanogaster stellate genes and
RT   their transcripts.";
RL   Genetics 124:303-316(1990).
CC   -!- FUNCTION: RESPONSIBLE FOR THE APPEARANCE OF PROTEINACEOUS STAR-
CC       SHAPED CRYSTALS IN THE PRIMARY SPERMATOCYTES OF D.MELANOGASTER
CC       MALES LACKING A Y CHROMOSOME.
CC   -!- MISCELLANEOUS: THERE ARE MULTIPLE COPIES OF THE STELLATE GENE IN
```

```
CC       FRUIT FLY.
CC   -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X15899; CAA33906.1; -.
DR   PIR; S08120; S08120.
DR   PIR; S24397; S24397.
DR   FlyBase; FBgn0003523; Ste.
DR   InterPro; IPR000704; CAS_kinase_II.
DR   Pfam; PF01214; CK_II_beta; 1.
DR   PRINTS; PR00472; CASNKINASEII.
DR   PROSITE; PS01101; CK2_BETA; 1.
KW   Testis; Multigene family.
SQ   SEQUENCE   172 AA;  19507 MW;  C86304F591E76F8A CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db      46 EILDV 50


RESULT   5
YA50_METJA
ID   YA50_METJA     STANDARD;      PRT;   177 AA.
AC   Q58450;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein MJ1050.
GN   MJ1050.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC   Methanococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   -!- SIMILARITY: BELONGS TO THE UPF0101 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U67548; AAB99053.1; -.
DR   TIGR; MJ1050; -.
KW   Hypothetical protein; ATP-binding; Complete proteome.
FT   NP_BIND       7     14       ATP (POTENTIAL).
SQ   SEQUENCE   177 AA;  20690 MW;  F209572AA79CD2F9 CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 177;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db     118 EILDV 122


RESULT   6
IFE2_ARATH
ID   IFE2_ARATH     STANDARD;      PRT;   198 AA.
AC   O04663; Q9SAN8;
DT   15-JUL-1998 (Rel. 36, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Eukaryotic translation initiation factor 4E (eIF-4E) (eIF4E) (mRNA
DE   cap-binding protein) (eIF-(iso)4F 25 kDa subunit) (eIF-(ISO)4F P28
DE   subunit) (eIF4Eiso protein).
GN   EIF4E2 OR AT5G35620 OR MJE4.8.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97378268; PubMed=9234949;
RA   Wittmann S., Chatel H., Fortin M.G., Laliberte J.F.;
RT   "Interaction of the viral protein genome linked of turnip mosaic
RT   potyvirus with the translational eukaryotic initiation factor (iso)
RT   4E of Arabidopsis thaliana using the yeast two-hybrid system.";
RL   Virology 234:84-92(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Rodriguez C., Freire M.A., Robaglia C.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=98403884; PubMed=9734815;
RA   Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT   Sequence features of the regions of 1,367,185 bp covered by 19
RT   physically assigned P1 and TAC clones.";
RL   DNA Res. 5:203-216(1998).
CC   -!- FUNCTION: RECOGNIZES AND BINDS THE 7-METHYLGUANOSINE-CONTAINING
CC       MRNA "CAP" DURING AN EARLY STEP IN THE INITIATION OF PROTEIN
CC       SYNTHESIS AND FACILITATES RIBOSOME BINDING BY INDUCING THE
CC       UNWINDING OF THE MRNAS SECONDARY STRUCTURES (BY SIMILARITY).
CC   -!- SUBUNIT: EIF4F IS A TRIMER COMPOSED OF EIF4E, EIF4G AND EIF4A
CC       (WHICH CAN CYCLE IN AND OUT OF THE COMPLEX). IN HIGHER PLANTS TWO
CC       ISOFORMS OF EIF4F HAVE BEEN IDENTIFIED, NAMED EIF4F AND
CC       EIF(ISO)4F. EIF4F HAS SUBUNITS P220 AND P28, WHEREAS EIF-(ISO)4F
CC       HAS SUBUNITS P82 AND P26 (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U62044; AAB66906.1; ALT_INIT.
DR   EMBL; Y10547; CAA71579.1; -.
DR   EMBL; AB013393; BAB09303.1; -.
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DR   HSSP; P07260; 1AP8.
DR   InterPro; IPR001040; eIF_4E.
DR   Pfam; PF01652; IF4E; 1.
DR   ProDom; PD003697; eIF_4E; 1.
DR   PROSITE; PS00813; IF4E; 1.
KW   Initiation factor; Protein biosynthesis; RNA-binding;
KW   Multigene family.
SQ   SEQUENCE   198 AA;  22514 MW;  71FEB309E073A9D2 CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 198;
  Best Local Similarity   100.0%;  Pred. No. 95;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db     175 EILDV 179


RESULT   7
NODB_RHIME
ID   NODB_RHIME     STANDARD;      PRT;   217 AA.
AC   P02963; O52477;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Chitooligosaccharide deacetylase (EC 3.5.1.-) (Nodulation protein B).
GN   NODB OR RA0474 OR SMA0868.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OG   Plasmid pSymA (megaplasmid 1).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=85229955; PubMed=4006668;
RA   Egelhoff T.T., Fisher R.F., Jacobs T.W., Mulligan J.T., Long S.R.;
RT   "Nucleotide sequence of Rhizobium meliloti 1021 nodulation genes:
RT   nodD is read divergently from nodABC.";
RL   DNA 4:241-248(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=41;
RX   MEDLINE=85087953; PubMed=6336331;
RA   Toeroek I., Kondorosi E., Stepkowski T., Posfai J., Kondorosi A.;
RT   "Nucleotide sequence of Rhizobium meliloti nodulation genes.";
RL   Nucleic Acids Res. 12:9509-9524(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=042B;
RA   Yang X., Gao W.M., Yang S.S.;
RT   "The complete sequence of S. meliloti 042B nodABC.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21396509; PubMed=11481432;
RA   Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA   Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA   Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA   Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA   Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT   "Nucleotide sequence and predicted functions of the entire
RT   Sinorhizobium meliloti pSymA megaplasmid.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
CC   -!- FUNCTION: IS INVOLVED IN GENERATING A SMALL HEAT-STABLE COMPOUND
CC       (NOD), AN ACYLATED OLIGOMER OF N-ACETYLGLUCOSAMINE, THAT
CC       STIMULATES MITOSIS IN VARIOUS PLANT PROTOPLASTS.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: TO OTHER POLYSACCHARIDE DEACETYLASES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M11268; AAA98361.1; -.
DR   EMBL; X01649; CAA25809.1; -.
DR   EMBL; AF038577; AAB95330.1; -.
DR   EMBL; AE007237; AAK65132.1; -.
DR   PIR; A03483; ZZZRBM.
DR   PIR; A03484; ZZZRB4.
DR   InterPro; IPR002509; Polysac_deacet.
DR   Pfam; PF01522; Polysac_deacet; 1.
KW   Hydrolase; Nodulation; Plasmid; Complete proteome.
FT   VARIANT      10     10       V -> M (IN STRAIN 41).
FT   VARIANT      59     59       A -> T (IN STRAIN 41).
FT   VARIANT     116    116       H -> R (IN STRAIN 41).
FT   VARIANT     195    198       ALSR -> GFPV (IN STRAIN O42B).
FT   CONFLICT    108    118       ACPQAAVRHIR -> LVLRPRSDTYE (IN REF. 1).
SQ   SEQUENCE   217 AA;  23671 MW;  01F82A0C75EA662D CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 217;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db      38 EILDV 42


RESULT   8
ACHP_LYMST
ID   ACHP_LYMST     STANDARD;      PRT;   229 AA.
AC   P58154;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetylcholine-binding protein precursor (ACh-binding protein) (AchBP).
OS   Lymnaea stagnalis (Great pond snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC   Lymnaeidae; Lymnaea.
OX   NCBI_TaxID=6523;
RN   [1]
RP   SEQUENCE FROM N.A., SEQUENCE OF 20-30, AND MASS SPECTROMETRY.
RC   TISSUE=CNS;
RX   MEDLINE=21256198; PubMed=11357121;
RA   Smit A.B., Syed N.I., Schaap D., van Minnen J., Klumperman J.,
RA   Kits K.S., Lodder H., van Der Schors R.C., van Elk R., Sorgedrager B.,
RA   Brejc K., Sixma T.K., Geraerts W.P.M.;
RT   "A glia-derived acetylcholine-binding protein that modulates synaptic
RT   transmission.";
RL   Nature 411:261-268(2001).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 20-229.
RX   MEDLINE=21256199; PubMed=11357122;
RA   Brejc K., van Dijk W.J., Klaassen R.V., Schuurmans M.,
RA   van Der Oost J., Smit A.B., Sixma T.K.;
RT   "Crystal structure of an ACh-binding protein reveals the
RT   ligand-binding domain of nicotinic receptors.";
RL   Nature 411:269-276(2001).
CC   -!- FUNCTION: BINDS TO ACETYLCHOLINE. MODULATES NEURONAL SYNAPTIC
CC       TRANSMISSION.
CC   -!- SUBUNIT: HOMOPENTAMER.
CC   -!- SUBCELLULAR LOCATION: SECRETED. RELEASED IN AN ACETYLCHOLINE-
CC       DEPENDENT MANNER IN THE SYNAPTIC CLEFT.
CC   -!- TISSUE SPECIFICITY: EXPRESSED BY GLIAL CELLS.
CC   -!- PTM: N-GLYCOSYLATED.
CC   -!- MASS SPECTROMETRY: MW=24720.4; METHOD=QTOF; RANGE=20-229.
CC   -!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF LIGAND-GATED IONIC
CC       CHANNELS FAMILY.
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CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF364899; AAK64377.1; -.
DR   PDB; 1I9B; 16-MAY-01.
KW   Glycoprotein; Signal; 3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    229       ACETYLCHOLINE-BINDING PROTEIN.
FT   DISULFID    142    155
FT   DISULFID    207    207
FT   CARBOHYD     85     85       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   229 AA;  26061 MW;  B76A3A13E7EF8FCB CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    191 EILDV 195


RESULT   9
DJBA_MOUSE
ID   DJBA_MOUSE     STANDARD;      PRT;   259 AA.
AC   Q9QYI5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DnaJ homolog subfamily B member 10 (mDJ8).
GN   DNAJB10.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=21023480; PubMed=11147971;
RA   Ohtsuka K., Hata M.;
RT   "Mammalian HSP40/DNAJ homologs: cloning of novel cDNAs and a proposal
RT   for their classification and nomenclature.";
RL   Cell Stress Chaperones 5:98-112(2000).
CC   -!- SIMILARITY: CONTAINS 1 J DOMAIN.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AB028858; BAA88306.1; -.
DR   HSSP; P25685; 1HDJ.
DR   MGD; MGI:1928739; Dnajb10.
DR   InterPro; IPR001623; DnaJ_N.
DR   InterPro; IPR002950; Josephin.
DR   InterPro; IPR003903; UIM.
DR   Pfam; PF00226; DnaJ; 1.
DR   Pfam; PF02809; UIM; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS00636; DNAJ_1; FALSE_NEG.
DR   PROSITE; PS50076; DNAJ_2; 1.
KW   Chaperone.
FT   DOMAIN        3     71       J-DOMAIN.
FT   DOMAIN      133    140       POLY-SER.
SQ   SEQUENCE   259 AA;  28601 MW;  81387B09ADF9B09A CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      6 EILDV 10


RESULT  10
NASD_KLEPN
ID   NASD_KLEPN     STANDARD;      PRT;   262 AA.
AC   P39459;
DT   01-FEB-1995 (Rel. 31, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Nitrate transport protein nasD.
GN   NASD.
OS   Klebsiella pneumoniae.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Klebsiella.
OX   NCBI_TaxID=573;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=M5A1;
RX   MEDLINE=94222832; PubMed=8169203;
RA   Lin J.T., Goldman B.S., Stewart V.;
RT   "The nasFEDCBA operon for nitrate and nitrite assimilation in
RT   Klebsiella pneumoniae M5al.";
RL   J. Bacteriol. 176:2551-2559(1994).
RN   [2]
RP   REVISIONS.
RC   STRAIN=M5A1;
RA   Stewart V.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROBABLY PART OF A HIGH-AFFINITY BINDING-PROTEIN-
CC       DEPENDENT TRANSPORT SYSTEM FOR NITRATE. PROBABLY RESPONSIBLE FOR
CC       ENERGY COUPLING TO THE TRANSPORT SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; L27431; AAB86901.1; -.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR001687; ATP_GTP_A.
DR   Pfam; PF00005; ABC_tran; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   Transport; ATP-binding; Membrane; Nitrate assimilation.
FT   NP_BIND      41     48       ATP (POTENTIAL).
SQ   SEQUENCE   262 AA;  28996 MW;  AD1B32490A2AEA10 CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    222 EILDV 226
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RESULT  11
YFAU_ECOLI
ID   YFAU_ECOLI     STANDARD;      PRT;   267 AA.
AC   P76469; P76925; P76926; P76928; P76929;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein yfaU.
GN   YFAU OR B2245.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97349980; PubMed=9205837;
RA   Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA   Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA   Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA   Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
RA   Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA   Yamagata S., Horiuchi T.;
RT   "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT   -K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT   analysis of its sequence features.";
RL   DNA Res. 4:91-113(1997).
CC   -!- SIMILARITY: BELONGS TO THE HPCH/HPAI ALDOLASE FAMILY.
CC   -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC       FRAMESHIFT IN POSITION 117.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE000314; AAC75305.1; -.
DR   EMBL; D90855; BAA16064.1; -.
DR   EMBL; D90855; BAA16065.1; ALT_FRAME.
DR   EMBL; D90856; CAB22004.1; ALT_FRAME.
DR   EMBL; D90856; CAB22003.1; ALT_FRAME.
DR   EcoGene; EG14083; yfaU.
KW   Hypothetical protein; Lyase; Complete proteome.
SQ   SEQUENCE   267 AA;  28916 MW;  F68506D8A11D23FE CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db     163 EILDV 167


RESULT  12
PURR_LACLA
ID   PURR_LACLA     STANDARD;      PRT;   271 AA.
AC   O53065;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Pur operon repressor.
GN   PURR OR LL2259.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and
OS   Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Lactococcus.
OX   NCBI_TaxID=1360, 1359;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=L.l.lactis; STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=L.l.cremoris; STRAIN=MG1363;
RA   Kilstrup M.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CONTROLS TRANSCRIPTION OF THE PUR OPERON FOR PURINE
CC       BIOSYNTHETIC GENES (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC       PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ222642; CAA10902.1; -.
DR   EMBL; AE006455; AAK06357.1; -.
DR   InterPro; IPR000836; Pribosyltran.
DR   Pfam; PF00156; Pribosyltran; 1.
DR   PROSITE; PS00103; PUR_PYR_PR_TRANSFER; FALSE_NEG.
KW   DNA-binding; Transcription regulation; Repressor; Complete proteome.
SQ   SEQUENCE   271 AA;  30361 MW;  04614AA24E1C4BCD CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db     148 EILDV 152


RESULT  13
ATPG_BACP3
ID   ATPG_BACP3     STANDARD;      PRT;   286 AA.
AC   P09222;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   ATP synthase gamma chain precursor (EC 3.6.3.14).
GN   ATPG.
OS   Bacillus PS3 (Thermophilic bacterium PS-3).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=70306;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88163679; PubMed=2894854;
RA   Ohta S., Yohda M., Ishizuka M., Hirata H., Hamamoto T.,
RA   Otawara-Hamamoto Y., Matsuda K., Kagawa Y.;
```

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RT   "Sequence and over-expression of subunits of adenosine triphosphate
RT   synthase in thermophilic bacterium PS3.";
RL   Biochim. Biophys. Acta 933:141-155(1988).
CC   -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC       GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
CC       IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
CC       THROUGH THE CF(0) COMPLEX.
CC   -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC       CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC       SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC       HAS THREE MAIN SUBUNITS: A, B AND C.
CC   -!- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07804; CAA30653.1; -.
DR   PIR; S01402; S01402.
DR   HSSP; P05631; 1BMF.
DR   InterPro; IPR000131; ATPase_gamma.
DR   Pfam; PF00231; ATP-synt; 1.
DR   PRINTS; PR00126; ATPASEGAMMA.
DR   PROSITE; PS00153; ATPASE_GAMMA; 1.
KW   Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport.
FT   PROPEP          1      4
FT   CHAIN           5    286       ATP SYNTHASE GAMMA CHAIN.
SQ   SEQUENCE   286 AA;  32248 MW;  A8B96F687C999252 CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 286;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    212 EILDV 216


RESULT  14
ATPG_BACCA
ID   ATPG_BACCA     STANDARD;      PRT;   287 AA.
AC   P41010;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   ATP synthase gamma chain (EC 3.6.3.14).
GN   ATPG.
OS   Bacillus caldotenax.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1395;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ishizuka M.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC       GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
CC       IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
CC       THROUGH THE CF(0) COMPLEX.
CC   -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC       CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC       SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC       HAS THREE MAIN SUBUNITS: A, B AND C.
CC   -!- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D38058; BAA07247.1; -.
DR   HSSP; P05631; 1BMF.
DR   InterPro; IPR000131; ATPase_gamma.
DR   Pfam; PF00231; ATP-synt; 1.
DR   PRINTS; PR00126; ATPASEGAMMA.
DR   PROSITE; PS00153; ATPASE_GAMMA; FALSE_NEG.
KW   ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase.
SQ   SEQUENCE   287 AA;  32343 MW;  BA039503BD1F1E5A CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    213 EILDV 217


RESULT  15
ATPG_BACST
ID   ATPG_BACST     STANDARD;      PRT;   287 AA.
AC   P42007;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   ATP synthase gamma chain (EC 3.6.3.14).
GN   ATPG.
OS   Bacillus stearothermophilus.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Geobacillus.
OX   NCBI_TaxID=1422;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ishizuka M., Imai H.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC       GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
CC       IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
CC       THROUGH THE CF(0) COMPLEX.
CC   -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC       CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC       SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC       HAS THREE MAIN SUBUNITS: A, B AND C.
CC   -!- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D38060; BAA07254.1; -.
DR   HSSP; P05631; 1BMF.
DR   InterPro; IPR000131; ATPase_gamma.
DR   Pfam; PF00231; ATP-synt; 1.
DR   PRINTS; PR00126; ATPASEGAMMA.
DR   PROSITE; PS00153; ATPASE_GAMMA; FALSE_NEG.
KW   ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase.
SQ   SEQUENCE   287 AA;  32391 MW;  78A9FB92E01BAE6E CRC64;


  Query Match             100.0%;  Score 23;  DB 1;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1 eildv 5
           |||||
Db     213 EILDV 217
```

Search completed: June 10, 2002, 06:24:23
Job time: 228 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:23:50 ; Search time 25.42 Seconds
(without alignments)
34.027 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	100.0	14	10	P82341	P82341 pisum sativ
2	23	100.0	50	16	Q9Z7L9	Q9z719 chlamydia p
3	23	100.0	70	3	Q9C2D4	Q9c2d4 neurospora
4	23	100.0	100	11	Q9D4R8	Q9d4r8 mus musculu
5	23	100.0	116	11	Q9JKS1	Q9jks1 rattus norv
6	23	100.0	117	11	Q9JKS2	Q9jks2 rattus norv
7	23	100.0	117	11	Q9JKS0	Q9jks0 rattus norv
8	23	100.0	117	11	Q9JKR8	Q9jkr8 rattus norv
9	23	100.0	119	17	O28742	O28742 archaeoglob
10	23	100.0	119	17	Q9HQG9	Q9hqg9 halobacteri
11	23	100.0	147	16	O53866	O53866 mycobacteri
12	23	100.0	171	3	Q9US90	Q9us90 schizosacch
13	23	100.0	172	5	Q9NIV2	Q9niv2 drosophila
14	23	100.0	174	16	Q97IB1	Q97ib1 clostridium
15	23	100.0	176	2	Q9F2I3	Q9f2i3 streptococc
16	23	100.0	180	2	Q9Z3N7	Q9z3n7 rhizobium s
17	23	100.0	180	16	Q97QD9	Q97qd9 streptococc
18	23	100.0	186	6	Q9MZ31	Q9mz31 bos taurus
19	23	100.0	200	10	Q9STJ1	Q9stj1 arabidopsis
20	23	100.0	208	3	O13501	O13501 phanerochae
21	23	100.0	212	4	O95609	O95609 homo sapien
22	23	100.0	219	2	Q53253	Q53253 rhizobium t
23	23	100.0	222	16	Q9WY98	Q9wy98 thermotoga
24	23	100.0	226	2	Q9L6U6	Q916u6 pseudomonas
25	23	100.0	242	17	Q27260	O27260 methanother
26	23	100.0	246	2	Q9FDJ6	Q9fdj6 lactobacill
27	23	100.0	253	16	O51655	O51655 borrelia bu
28	23	100.0	256	5	O44520	O44520 caenorhabdi
29	23	100.0	266	16	Q92ZZ3	Q92zz3 rhizobium m
30	23	100.0	267	17	Q97WL9	Q97wl9 sulfolobus
31	23	100.0	268	10	Q94BW7	Q94bw7 cicer ariet
32	23	100.0	270	2	O24845	O24845 acinetobact
33	23	100.0	271	4	Q9H027	Q9h027 homo sapien
34	23	100.0	271	16	O53065	O53065 lactococcus
35	23	100.0	274	11	Q9EQ23	Q9eq23 rattus norv
36	23	100.0	277	11	Q921S2	Q921s2 mus musculu
37	23	100.0	282	2	Q52412	Q52412 thermophili
38	23	100.0	287	16	Q9CN70	Q9cn70 pasteurella
39	23	100.0	289	16	Q92H07	Q92h07 rickettsia
40	23	100.0	290	5	O17829	O17829 caenorhabdi
41	23	100.0	307	16	Q9JUD6	Q9jud6 neisseria m
42	23	100.0	307	16	Q9JS34	Q9js34 neisseria m
43	23	100.0	308	2	Q9X9K3	Q9x9k3 vibrio para
44	23	100.0	312	3	O74864	O74864 schizosacch
45	23	100.0	317	6	Q9GMV1	Q9gmv1 macaca fasc

ALIGNMENTS

RESULT 1
P82341
ID P82341 PRELIMINARY; PRT; 14 AA.
AC P82341;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF THYLAKOID (SPOT251) (FRAGMENT).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of lumenal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5, ITS MW IS: 16.9 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1590 MW; 6D968D2994D0185B CRC64;

Query Match 100.0%; Score 23; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 7 EILDV 11

```
RESULT   2
Q9Z7L9
ID   Q9Z7L9      PRELIMINARY;      PRT;    50 AA.
AC   Q9Z7L9;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   HYPOTHETICAL 6.0 KDA PROTEIN.
GN   CPN0685 OR CPJ0685.
OS   Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX   NCBI_TaxID=83558;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CWL029;
RX   MEDLINE=99206606; PubMed=10192388;
RA   Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA   Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT   "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL   Nat. Genet. 21:385-389(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=J138;
RX   MEDLINE=20330349; PubMed=10871362;
RA   Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA   Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT   "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT   from Japan and CWL029 from USA.";
RL   Nucleic Acids Res. 28:2311-2314(2000).
DR   EMBL; AE001651; AAD18824.1; -.
DR   EMBL; AP002547; BAA98892.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   50 AA;  5959 MW;  4A8961A037A16495 CRC64;

  Query Match             100.0%;  Score 23;  DB 16;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db       7 EILDV 11


RESULT   3
Q9C2D4
ID   Q9C2D4      PRELIMINARY;      PRT;    70 AA.
AC   Q9C2D4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 7.8 KDA PROTEIN.
GN   9G6.310.
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA   Nyakatura G., Mewes H.W., Mannhaupt G.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   German Neurospora genome project;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL513463; CAC28779.2; -.
KW   Hypothetical protein.
SQ   SEQUENCE   70 AA;  7809 MW;  ED4EC64FE6B2E9BC CRC64;

  Query Match             100.0%;  Score 23;  DB 3;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db       7 EILDV 11


RESULT   4
Q9D4R8
ID   Q9D4R8      PRELIMINARY;      PRT;   100 AA.
AC   Q9D4R8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   4930568L21RIK PROTEIN.
GN   4930568L21RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TESTIS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK016255; BAB30165.1; -.
DR   MGD; MGI:1923108; 4930568L21Rik.
SQ   SEQUENCE   100 AA;  11528 MW;  59CFB27CD19C1112 CRC64;

  Query Match             100.0%;  Score 23;  DB 11;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db      93 EILDV 97


RESULT   5
Q9JKS1
ID   Q9JKS1      PRELIMINARY;      PRT;   116 AA.
AC   Q9JKS1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   MUTANT C-KIT RECEPTOR (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=BROWN NORWAY; TISSUE=TESTIS;
RA   Gangadharan S., Ali S.;
RT   "RT-PCR generated mRNA transcript from proven infertile Brown Norway
RT   male rat testis.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF228308; AAF69131.1; -.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12583 MW;  8BDA5FB24E2471EC CRC64;


  Query Match             100.0%;  Score 23;  DB 11;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     75 EILDV 79


RESULT   6
Q9JKS2
ID   Q9JKS2      PRELIMINARY;      PRT;   117 AA.
AC   Q9JKS2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   C-KIT RECEPTOR (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BROWN NORWAY; TISSUE=TESTIS, AND BRAIN;
RA   Gangadharan S., Ali S.;
RT   "RT-PCR generated mRNA transcript from proven infertile Brown Norway
RT   male rat testis.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF228307; AAF69130.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   SMART; SM00410; IG_like; 1.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12635 MW;  E2141AF47115EE78 CRC64;


  Query Match             100.0%;  Score 23;  DB 11;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     76 EILDV 80


RESULT   7
Q9JKS0
ID   Q9JKS0      PRELIMINARY;      PRT;   117 AA.
AC   Q9JKS0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   C-KIT RECEPTOR (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BROWN NORWAY; TISSUE=TESTIS;
RA   Gangadharan S., Ali S.;
RT   "RT-PCR generated mRNA transcript from proven infertile Brown Norway
RT   male rat testis.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF228309; AAF69132.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   SMART; SM00410; IG_like; 1.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12611 MW;  E7BEC87E579CB678 CRC64;


  Query Match             100.0%;  Score 23;  DB 11;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     76 EILDV 80


RESULT   8
Q9JKR8
ID   Q9JKR8      PRELIMINARY;      PRT;   117 AA.
AC   Q9JKR8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   C-KIT RECEPTOR (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BROWN NORWAY; TISSUE=TESTIS;
RA   Gangadharan S., Ali S.;
RT   "RT-PCR generated mRNA transcript from proven infertile Brown Norway
RT   male rat testis.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF228311; AAF69134.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   SMART; SM00410; IG_like; 1.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12641 MW;  F3FBDC2F1288F378 CRC64;


  Query Match             100.0%;  Score 23;  DB 11;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     76 EILDV 80


RESULT   9
O28742
ID   O28742      PRELIMINARY;      PRT;   119 AA.
AC   O28742;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   CONSERVED HYPOTHETICAL PROTEIN.
GN   AF1530.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC   Archaeoglobus.
OX   NCBI_TaxID=2234;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
DR   EMBL; AE000997; AAB89718.1; -.
DR   TIGR; AF1530; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   119 AA;  14025 MW;  7F75DA993E80C15C CRC64;


  Query Match             100.0%;  Score 23;  DB 17;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    109 EILDV 113


RESULT  10
Q9HQG9
ID   Q9HQG9      PRELIMINARY;      PRT;   119 AA.
AC   Q9HQG9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VNG1169C.
GN   VNG1169C.
OS   Halobacterium sp. (strain NRC-1).
OC   Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC   Halobacterium.
OX   NCBI_TaxID=64091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20504483; PubMed=11016950;
RA   Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA   Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA   Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA   Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA   Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA   Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA   Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA   Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT   "Genome sequence of Halobacterium species NRC-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97;12176-12181(2000).
DR   EMBL; AE005045; AAG19546.1; -.
KW   Complete proteome.
SQ   SEQUENCE   119 AA;  13648 MW;  585905ABA983B9B1 CRC64;


  Query Match             100.0%;  Score 23;  DB 17;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    110 EILDV 114


RESULT  11
O53866
ID   O53866      PRELIMINARY;      PRT;   147 AA.
AC   O53866;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 16.3 KDA PROTEIN.
GN   RV0854 OR MTV043.47.
OS   Mycobacterium tuberculosis.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37RV;
RX   MEDLINE=98295987; PubMed=9634230;
RA   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA   Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA   Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA   Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA   Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA   Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA   Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA   Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT   "Deciphering the biology of Mycobacterium tuberculosis from the
RT   complete genome sequence.";
RL   Nature 393:537-544(1998).
DR   EMBL; AL022004; CAA17660.1; -.
DR   TubercuList; Rv0854; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   147 AA;  16345 MW;  D8B55F6B86293E07 CRC64;


  Query Match             100.0%;  Score 23;  DB 16;  Length 147;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     17 EILDV 21


RESULT  12
Q9US90
ID   Q9US90      PRELIMINARY;      PRT;   171 AA.
AC   Q9US90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL NUCLEAR PROTEIN (FRAGMENT).
GN   SPCC330.04C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=968 H90;
RX   MEDLINE=20223868; PubMed=10759889;
RA   Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA   Hiraoka Y.;
RT   "Large-scale screening of intracellular protein localization in living
RT   fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL   Genes Cells 5:169-190(2000).
DR   EMBL; AB027955; BAA87259.1; -.
KW   Nuclear protein.
FT   NON_TER       1      1
FT   NON_TER     171    171
SQ   SEQUENCE   171 AA;  21395 MW;  30012B18345508BE CRC64;
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```
  Query Match             100.0%;  Score 23;  DB 3;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db    151 EILDV 155


RESULT  13
Q9NIV2
ID   Q9NIV2      PRELIMINARY;      PRT;   172 AA.
AC   Q9NIV2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   STELLATE PROTEIN.
GN   STE.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shevelyov Y.Y., Kalmykova A.I.;
RT   "Stellate orphon provides a poly(A) signal for bendless mRNA.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF192309; AAF35172.1; -.
DR   FlyBase; FBgn0003523; Ste.
DR   InterPro; IPR000704; CAS_kinase_II.
DR   Pfam; PF01214; CK_II_beta; 1.
DR   PRINTS; PR00472; CASNKINASEII.
DR   PROSITE; PS01101; CK2_BETA; 1.
SQ   SEQUENCE   172 AA;  19525 MW;  A2C8752F3A976F8B CRC64;


  Query Match             100.0%;  Score 23;  DB 5;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     46 EILDV 50


RESULT  14
Q97IB1
ID   Q97IB1      PRELIMINARY;      PRT;   174 AA.
AC   Q97IB1;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   UNCHARACTERIZED CONSERVED PROTEIN (COILED-COIL).
GN   CAC1739.
OS   Clostridium acetobutylicum.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1488;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX   MEDLINE=21359325; PubMed=11466286;
RA   Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA   Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA   Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA   Bennett G.N., Koonin E.V., Smith D.R.;
RT   "Genome sequence and comparative analysis of the solvent-producing
RT   bacterium Clostridium acetobutylicum.";
RL   J. Bacteriol. 183:4823-4838(2001).
DR   EMBL; AE007683; AAK79705.1; -.
KW   Complete proteome.
SQ   SEQUENCE   174 AA;  20244 MW;  80EA9CA386E436BF CRC64;


  Query Match             100.0%;  Score 23;  DB 16;  Length 174;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     32 EILDV 36


RESULT  15
Q9F2I3
ID   Q9F2I3      PRELIMINARY;      PRT;   176 AA.
AC   Q9F2I3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   YLBN-LIKE HYPOTHETICAL PROTEIN.
GN   YLBN-LIKE.
OS   Streptococcus gordonii challis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=29390;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CHALLIS;
RA   Minick P., Vickerman M.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U12643; AAG32547.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   176 AA;  19929 MW;  B73E430114725CFF CRC64;


  Query Match             100.0%;  Score 23;  DB 2;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db     32 EILDV 36


Search completed: June 10, 2002, 06:28:04
Job time: 254 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:21:15 ; Search time 25.45 Seconds
(without alignments)
21.822 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	100.0	5	17	AAR95719	Alpha-4Beta-1 inte
2	23	100.0	5	18	AAW25192	LDV-peptide capabl
3	23	100.0	5	19	AAW46318	Peptide recognised
4	23	100.0	5	20	AAY03855	Integrin ligand di
5	23	100.0	5	21	AAY80488	Cell adhesion pept
6	23	100.0	5	21	AAY77442	Fibronectin CS1-de
7	23	100.0	5	21	AAY69619	VLA-4 inhibitor pe
8	23	100.0	5	22	AAB73465	Fibronectin VLA-4
9	23	100.0	5	22	AAB91966	Fibronectin fragme
10	23	100.0	5	22	AAB50876	Integrin recogniti
11	23	100.0	5	22	AAB59135	Peptide #3 recogni
12	23	100.0	6	21	AAY77443	Fibronectin CS1-de
13	23	100.0	6	21	AAY77444	Fibronectin CS1-de
14	23	100.0	7	19	AAW56065	Alpha4 integrins t
15	23	100.0	8	12	AAR11361	Peptide #352 deriv
16	23	100.0	8	13	AAR28885	Cell adhesion inhi
17	23	100.0	8	15	AAR44360	Polymer-bound cell
18	23	100.0	8	17	AAR92536	VLA-4 binding pept
19	23	100.0	8	18	AAW25190	LDV-peptide capabl
20	23	100.0	8	19	AAW63133	Peptide sequence o
21	23	100.0	8	19	AAW56046	Chimeric adenoviru
22	23	100.0	8	20	AAY32862	Fibronectin protei
23	23	100.0	8	20	AAY32874	Fibronectin protei
24	23	100.0	8	21	AAB35734	Vitronectin peptid
25	23	100.0	8	21	AAY80489	Cell adhesion pept
26	23	100.0	8	21	AAY69618	VLA-4 inhibitor pe
27	23	100.0	8	22	AAB73464	Fibronectin VLA-4
28	23	100.0	8	22	AAB91967	Fibronectin fragme
29	23	100.0	9	13	AAR29631	Adhesion inhibitor
30	23	100.0	9	13	AAR30433	Cell adhesion inhi
31	23	100.0	9	13	AAR28886	Cell adhesion inhi
32	23	100.0	9	21	AAY77436	Fibronectin CS1-de
33	23	100.0	9	21	AAY77437	Fibronectin CS1-de
34	23	100.0	9	21	AAY77438	Fibronectin CS1-de
35	23	100.0	9	21	AAY77439	Fibronectin CS1-de
36	23	100.0	10	13	AAR25998	Adhesion inhibitor
37	23	100.0	10	13	AAR30432	Cell adhesion inhi
38	23	100.0	10	13	AAR29103	Platelet aggregati
39	23	100.0	10	13	AAR29105	Platelet aggregati
40	23	100.0	10	13	AAR29106	Platelet aggregati
41	23	100.0	10	13	AAR29107	Platelet aggregati
42	23	100.0	10	13	AAR29108	Platelet aggregati
43	23	100.0	10	13	AAR29109	Platelet aggregati
44	23	100.0	10	16	AAW01705	Standard peptide f
45	23	100.0	10	16	AAW01725	Inhibitor of fibro

ALIGNMENTS

RESULT 1
AAR95719
ID AAR95719 standard; peptide; 5 AA.
XX
AC AAR95719;
XX
DT 04-DEC-1996 (first entry)
XX
DE Alpha-4Beta-1 integrin binding inhibitory peptide 16.
XX
KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW inhibitor; binding; white blood cell; migration; capillary wall;
KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW CS1; CS5; H1; LDV; active site.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 5
FT /note= "Val-NH2"
XX
PN US5510332-A.
XX
PD 23-APR-1996.
XX
PF 07-JUL-1994; 94US-0271830.
XX
PR 07-JUL-1994; 94US-0271830.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Beck PJ, Kogan TP, Ren K, Vanderslice P;
XX
DR WPI; 1996-221274/22.

XX
PT New peptide(s) based on the LDV domain of fibronectin - used for
PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT fibronectin or invasin
XX
PS Disclosure; Column 21-22; 35pp; English.
XX
CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
CC surface of endothelial cells that line the interior wall of capillaries.
CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
CC white blood cells to adhere to the capillary wall in areas where the
CC tissue surrounding the capillary has been infected or damaged. Sometimes
CC this white blood cell migration can become uncontrolled, with white
CC blood cells flooding to the scene, causing widespread tissue damage.
CC Cpds. capable of blocking this process may be beneficial as therapeutic
CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC fibronectin. Three distinct IA4B1-binding sites have been identified
CC within fibronectin. One site is found in the HeplI region and is
CC expressed in all isoforms; two others (CS1 and CS5) are present in the
CC alternatively spliced type III connecting segments. CS1 has the higher
CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC peptide that include the LDV domain presented in such a way by its novel
CC flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 2
AAW25192
ID AAW25192 standard; peptide; 5 AA.
XX
AC AAW25192;
XX
DT 05-JAN-1998 (first entry)
XX
DE LDV-peptide capable of binding cell adhesion molecules.
XX
KW LDV; leucine; aspartic acid; valine; cell adhesion molecule;
KW binding; bladder irrigation; tumour removal; endoscopic operation;
KW transurethral resection; cancer; neoplasia.
XX
OS Synthetic.
XX
PN DE19529909-A1.
XX
PD 20-FEB-1997.
XX
PF 15-AUG-1995; 95DE-1029909.
XX
PR 15-AUG-1995; 95DE-1029909.
XX
PA (FREP) FRESENIUS AG.
XX
PI Boehle A;
XX
DR WPI; 1997-133793/13.
XX
PT Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
PT adhesion molecules
XX
PS Claim 6; Page 8; 8pp; German.
XX
CC AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
CC The peptides are capable of binding to cell adhesion molecules and
CC are used in aqueous irrigation solutions for use during and after
CC endoscopic operations. Preferred irrigation solutions are
CC electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
CC oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
CC GPRP, VTL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid
CC code). The solutions are especially used for irrigating the bladder
CC during and after tumour removal by transurethral resection. The
CC peptides protect against recurrence of tumours.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 3
AAW46318
ID AAW46318 standard; Protein; 5 AA.
XX
AC AAW46318;
XX
DT 08-MAY-1998 (first entry)
XX
DE Peptide recognised by integrin alpha4eta1.
XX
KW Fibrinogen; integrin; alpha-IIb-beta3; cell surface receptor;
KW penton base protein; coat proteins; adenovirus; binding site;
KW cellular adhesion; extracellular matrix molecule; binding domain;
KW cell surface binding site; bispecific molecule; gene therapy.
XX
OS Unidentified.
XX
PN US5712136-A.
XX
PD 27-JAN-1998.
XX
PF 17-APR-1996; 96US-0634060.
XX
PR 08-SEP-1994; 94US-0303162.
XX
PA (GENV-) GENVEC INC.
XX
PI Brough DE, Bruder JT, Kovesdi I, McVey DL, Roelvink PW;
PI Wickham TJ;
XX
DR WPI; 1998-119984/11.
XX
PT Methods for introducing adenovirus into cells - used for genetic
PT engineering and gene therapy
XX
PS Claim 27; Column 2; 56pp; English.
XX
CC The present sequence is a linear stretch of amino acids (present in
CC fibronectin) recognised by the integrin alpha4beta1. Integrins are
CC cell surface receptors. The penton base protein (one of the coat
CC proteins) of adenoviruses binds to integrins. The integrins not only
CC provide a binding site for the adenoviral penton base protein, but also
CC mediate cellular adhesion to the extracellular matrix molecules. The
CC specification describes a method of introducing an adenovirus into
CC a cell in vitro having a particular cell surface binding site. The
CC adenovirus is contacted with a bispecific molecule comprising a component
CC that selectively binds a binding domain of the penton base protein of the
CC adenovirus and a second component that selectively binds the cell surface
CC binding site. A complex of the adenovirus and the bispecific molecule is

CC formed, and the cell is contacted with it to allow entry of the
CC adenovirus into the cell. The methods can be used for research and the
CC vectors can be used for gene therapy.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 4
AAY03855
ID AAY03855 standard; peptide; 5 AA.
XX
AC AAY03855;
XX
DT 16-JUN-1999 (first entry)
XX
DE Integrin ligand dissociator (ILD) peptide.
XX
KW Integrin-ligand; dissociator; disaggregation; platelet thrombus; stroke;
KW fibrinogen; glycoprotein IIb-IIIa; angina; myocardial infarction; bone;
KW osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy;
KW psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
KW organ transplant rejection; arthritis; ILD.
XX
OS Synthetic.
XX
PN WO9911280-A1.
XX
PD 11-MAR-1999.
XX
PF 03-SEP-1998; 98WO-US18305.
XX
PR 03-SEP-1997; 97US-0057463.
XX
PA (BURN-) BURNHAM INST.
XX
PI Hu DD, Smith JW;
XX
DR WPI; 1999-243586/20.
XX
PT Disaggregating a ligand:integrin receptor complex
XX
PS Disclosure; Page 10; 39pp; English.
XX
CC The invention relates to integrin ligand dissociators. Disaggregation of
CC an existing platelet thrombus in a blood vessel is due to dissociation of
CC fibrinogen from glycoprotein IIb-IIIa. This dissociation is caused by the
CC binding of an integrin-ligand dissociator at ligand binding site I of
CC glycoprotein IIb-IIIa. The invention provides a method of disaggregating
CC an existing platelet thrombus in a blood vessel, where the platelet
CC thrombus may form an occlusion of a blood vessel, in a subject comprises
CC administering a compound which dissociates fibrinogen bound to a first
CC site on platelet glycoprotein IIb-IIIa, by binding to a second
CC interacting site on platelet glycoprotein IIb-IIIa, disaggregating the
CC platelet thrombus. The method is used to treat humans with unstable
CC angina, stroke and/or acute myocardial infarction. The methods can be
CC used to enact de-adhesion of osteoclasts from the bone surface to halt
CC bone loss in a patient with osteoporosis. The methods can also be used
CC for the de-adhesion of angiogenic endothelial cells in a patient with a
CC pathologic condition associated with angiogenesis, e.g. cancer, diabetic
CC retinopathy, psoriasis. The methods can also be used to treat tumours,
CC atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory
CC bowel disease, or organ transplant rejection, and asthma. The methods can
CC be used for the dissolution of pre-formed platelet aggregates, which is a
CC departure from the current strategy of treatment prior to formation of
CC vascular occlusions. The present sequence represents an integrin ligand
CC dissociator (ILD) that can be used in the method of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 5
AAY80488
ID AAY80488 standard; peptide; 5 AA.
XX
AC AAY80488;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cell adhesion peptide #23.
XX
KW Bone regenerative; osteopathic; osseous tissue; reconstitution;
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.
XX
OS Synthetic.
XX
PN WO200004941-A1.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16800.
XX
PR 24-JUL-1998; 98US-0122348.
XX
PA (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
XX
PI Budny JA;
XX
DR WPI; 2000-195084/17.
XX
PT System for reconstructing osseous tissue, useful e.g. for treating
PT fractures, comprises scaffold containing promoter of bone formation and
PT inhibitor of bone resorption
XX
PS Claim 14; Page 32; 44pp; English.
XX
CC The invention relates to a novel system for reconstitution of osseous
CC tissue comprising a scaffold carrying a compound (I) that promotes
CC bone formation and a component that decreases bone resorption (II).
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular
CC matrix. (I) is preferably selected from: selectin or selectin binding
CC fragments, proteins and peptides that facilitate cell adhesion,
CC plasminogen activator inhibitors, protease inhibitors and
CC metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed
CC examples of cell adhesion peptides used in the system of the invention.
CC The system is used to replace, remodel or correct bone defects, e.g.
CC fractures, fissures or bone mass loss. Incorporation of (I) into the
CC scaffold results in rapid seeding by osteoblasts and the development of
CC an organic matrix, i.e. the preformed scaffold replaces the
CC rate-determining step of extracellular matrix formation. The scaffold can
CC be designed to have a predetermined resorption/degradation rate, and may
CC include regulatory compounds for specific cell types.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 21; Length 5;

```
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   6
AAY77442
ID   AAY77442 standard; peptide; 5 AA.
XX
AC   AAY77442;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Fibronectin CS1-derived peptide #33.
XX
KW   Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW   CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW   inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS   Mammalia.
XX
PN   WO200002903-A1.
XX
PD   20-JAN-2000.
XX
PF   15-DEC-1998;   98WO-US26605.
XX
PR   10-JUL-1998;   98US-0113689.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Arrhenius TS,  Elices MJ,  Gaeta FCA,  He Y,  Huyghe BG,  Chen PG;
XX
DR   WPI; 2000-182213/16.
XX
PT   New peptidomimetic compounds used as cell surface fibronectin
PT   expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT   cardiovascular disorders  -
XX
PS   Disclosure; Fig 2; 243pp; English.
XX
CC   The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC   capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC   CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC   the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC   the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC   important role in the maturation and trafficking. VLA-4-mediated
CC   leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC   critical step in the inflammatory response. The peptidomimetics of the
CC   invention may be used to treat both chronic and acute immunoinflammatory
CC   conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC   allograft rejection. They may also be used to treat psoriasis and other
CC   skin inflammations, demyelinating diseases of the central nervous system
CC   (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC   diabetes, inflammatory bowel disease, kidney inflammation and
CC   restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC   involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC   immune response on repeated administration, or the 25-mer CS-1 peptide,
CC   which is large and costly to make and is subject to rapid proteolytic
CC   degradation. The peptidomimetics of the invention are smaller in
CC   comparison to the CS-1 peptide and therefore less expensive to
CC   manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
CC   and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
CC   their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC   (AAY77410).
XX
SQ   Sequence   5 AA;


  Query Match           100.0%;  Score 23;  DB 21;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   7
AAY69619
ID   AAY69619 standard; peptide; 5 AA.
XX
AC   AAY69619;
XX
DT   19-APR-2000  (first entry)
XX
DE   VLA-4 inhibitor peptide #2.
XX
KW   LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1;
KW   CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative;
KW   arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder;
KW   autoimmune disorder; respiratory disorder; LDV motif.
XX
OS   Synthetic.
XX
PN   WO200000477-A1.
XX
PD   06-JAN-2000.
XX
PF   31-MAY-1999;   99WO-IB00973.
XX
PR   30-JUN-1998;   98US-0091180.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Duplantier AJ,  Milici AJ,  Chupak LS;
XX
DR   WPI; 2000-126762/11.
XX
PT   Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives  -
XX
PS   Disclosure; Page 2; 120pp; English.
XX
CC   The invention relates to novel arylalkyl and arylureidoalkyl
CC   azolylalkanoic acid derivatives and related compounds (I), and their
CC   salts and prodrugs. These are are integrin inhibitors, specifically of
CC   VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29),
CC   which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
CC   inducible cell surface protein VCAM-1 (vascular cell adhesion
CC   molecule-1) and for the alternatively spliced forms of fibronectin (FN)
CC   which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
CC   and consequent or associated pathogenic processes mediated by VLA-4, and
CC   may therefore be useful in the treatment and prevention of inflammatory,
CC   autoimmune, or respiratory disorders . These include asthma, arthritis,
CC   psoriasis, multiple sclerosis, transplant rejection, diabetes, and
CC   inflammatory bowel disease. Sequences AAY69618-Y69620 represent peptides
CC   derived from the VLA-4-binding domain of the FN CS-1 region which
CC   contain the LDV motif and are known to inhibit fibronectin-dependent
CC   cell adhesion.
XX
SQ   Sequence   5 AA;


  Query Match           100.0%;  Score 23;  DB 21;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   8
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```
AAB73465
ID   AAB73465 standard; peptide; 5 AA.
XX
AC   AAB73465;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Fibronectin VLA-4 binding domain-derived pentapeptide #1.
XX
KW   Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
KW   very late antigen; antibody; kidney disease; chronic renal failure;
KW   end-stage renal disease; chronic diabetic nephropathy;
KW   diabetic glomerulopathy; diabetic renal hypertrophy;
KW   hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
KW   chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
KW   nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
XX
OS   Unidentified.
XX
PN   WO200119396-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US25140.
XX
PR   14-SEP-1999;   99US-0153826.
XX
PA   (BIOJ ) BIOGEN INC.
PA   (UNLO ) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
XX
PI   Allen A,  Pusey C,  Lobb R;
XX
DR   WPI; 2001-273408/28.
XX
PT   Treating a mammal in, or at a risk of developing, chronic renal
PT   failure, involves administering at least one integrin antagonist to the
PT   mammal  -
XX
PS   Disclosure; Page 24; 62pp; English.
XX
CC   The invention relates to a method for treating a mammal with,
CC   or at risk of developing, chronic renal failure, involving the
CC   administration of at least one integrin antagonist. The integrin
CC   antagonists that may be used in the method include antagonists of
CC   alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
CC   containing integrins. In particular, the antagonists are antibodies
CC   specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
CC   VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
CC   integrin and its cognate ligand (collagen I, collagen IV, and laminin in
CC   the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).
CC   The method of the invention may be used to treat chronic renal failure,
CC   end-stage renal disease, chronic diabetic nephropathy, diabetic
CC   glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
CC   hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary
CC   nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
CC   peptides derived from the VLA-4 binding domain (CS-1 region) of
CC   fibronectin, which inhibit fibronectin-dependent cell adhesion, and may
CC   therefore be used in the method of the invention.
XX
SQ   Sequence   5 AA;

  Query Match             100.0%;  Score 23;  DB 22;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   9
AAB91966
ID   AAB91966 standard; Peptide; 5 AA.
XX
AC   AAB91966;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Fibronectin fragment and fibrin related peptide SEQ ID NO:1142.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US13576.
XX
PR   17-MAY-1999;   99US-0134406.
PR   10-SEP-1999;   99US-0153406.
PR   15-OCT-1999;   99US-0159783.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity
PT   -
XX
PS   Disclosure; Page 569; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity
CC   in vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention.
XX
SQ   Sequence   5 AA;

  Query Match             100.0%;  Score 23;  DB 22;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT  10
AAB50876
ID   AAB50876 standard; peptide; 5 AA.
XX
AC   AAB50876;
XX
```

```
DT   19-MAR-2001  (first entry)
XX
DE   Integrin recognition peptide sequence #3.
XX
KW   Integrin; transmembrane protein; alpha4 integrin inhibitor;
KW   paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
KW   multiple sclerosis; asthma; atherosclerosis; wound healing.
XX
OS   Unidentified.
XX
PN   WO200073342-A1.
XX
PD   07-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-US15153.
XX
PR   01-JUN-1999;   99US-0323447.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Ginsberg MH,  Pfaff M,  Liu S;
XX
DR   WPI; 2001-070959/08.
XX
PT   Polypeptides useful in construction of structural models for
PT   identifying therapeutic compounds, comprises series of heptad repeats
PT   that mimic a transmembrane domain and cytoplasmic domain attached to
PT   heptad repeats  -
XX
PS   Disclosure; Page 2; 37pp; English.
XX
CC   The present sequence is given in a specification relating to a
CC   polypeptide comprising a series of heptad-repeats that mimic a
CC   transmembrane domain, and a selected cytoplasmic domain attached to the
CC   heptad repeats. At least a portion of the polypeptide is prepared
CC   recombinantly or at least 1 heptad repeat in the series has a different
CC   amino acid sequence to other heptad repeats in the series. The
CC   polypeptide is useful in the construction of structural models which are
CC   useful for evaluating structure and activity of a selected occupied and
CC   clustered transmembrane protein having the selected cytoplasmic domain
CC   and for identifying therapeutic compounds. It is also useful for
CC   identifying agents as inhibitors of alpha4 integrin biological
CC   responses by contacting the structural model with paxillin or a
CC   paxillin related molecule in the presence and absence of a test agent
CC   and determining binding of paxillin or paxillin related molecule to the
CC   structural model. A decrease in binding in the presence of the test
CC   agent indicates that the test agent is an inhibitor of alpha4 integrin
CC   biological response. Inhibitors of the binding of paxillin to alpha4 are
CC   useful in blocking immune responses in conditions such as inflammatory
CC   bowel disease, arthritis, multiple sclerosis and asthma and in
CC   inhibiting atherosclerosis and scarring during wound healing.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 23;  DB 22;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT  11
AAB59135
ID   AAB59135 standard; peptide; 5 AA.
XX
AC   AAB59135;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Peptide #3 recognised by integrin.
XX
KW   Heptad repeat; transmembrane domain; cytoplasmic; integrin;
KW   inflammation; thrombosis; malignancy.
XX
OS   Synthetic.
XX
PN   WO200073341-A1.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14656.
XX
PR   27-MAY-1999;   99US-0320907.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Ginsberg MH,  Pfaff M;
XX
DR   WPI; 2001-041143/05.
XX
PT   Polypeptides useful in construction of structural models for
PT   identifying therapeutic compounds, comprises series of heptad repeats
PT   that mimic a transmembrane domain and cytoplasmic domain attached to
PT   the repeats  -
XX
PS   Disclosure; Page 2; 36pp; English.
XX
CC   The present invention relates to a peptide with a series of
CC   heptad-repeats that mimic a transmembrane domain and a selected
CC   cytoplasmic domain attached to the heptad repeats. The invention
CC   is useful for evaluating structure and activity of a selected
CC   occupied and clustered transmembrane protein with the selected
CC   cytoplasmic domain and for identifying therapeutic compounds. It
CC   is also useful for identifying a cytoplasmic domain binding partner.
CC   It is may be used to study protein interactions with transmembrane
CC   proteins such as integrin, which can be used to treat conditions in
CC   which over activity of integrins is involved, such as inflammation,
CC   thrombosis and malignancy.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 23;  DB 22;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT  12
AAY77443
ID   AAY77443 standard; peptide; 6 AA.
XX
AC   AAY77443;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Fibronectin CS1-derived peptide #34.
XX
KW   Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW   CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW   inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS   Mammalia.
XX
PN   WO200002903-A1.
XX
PD   20-JAN-2000.
XX
PF   15-DEC-1998;   98WO-US26605.
XX
```

PR 10-JUL-1998; 98US-0113689.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX
DR WPI; 2000-182213/16.
XX
PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders -
XX
PS Disclosure; Fig 2; 243pp; English.
XX
CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAY77410).
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 23; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 2 eildv 6

RESULT 13
AAY77444
ID AAY77444 standard; peptide; 6 AA.
XX
AC AAY77444;
XX
DT 22-MAY-2000 (first entry)
XX
DE Fibronectin CS1-derived peptide #35.
XX
KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS Mammalia.
XX
PN WO200002903-A1.
XX
PD 20-JAN-2000.
XX
PF 15-DEC-1998; 98WO-US26605.
XX

PR 10-JUL-1998; 98US-0113689.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX
DR WPI; 2000-182213/16.
XX
PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders -
XX
PS Disclosure; Fig 2; 243pp; English.
XX
CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAY77410).
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 23; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 14
AAW56065
ID AAW56065 standard; peptide; 7 AA.
XX
AC AAW56065;
XX
DT 29-JUL-1998 (first entry)
XX
DE Alpha4 integrins targeting sequence SEQ ID NO:80.
XX
KW Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
KW constrained peptide motif; gene therapy; cancer; heart disease;
KW autoimmune disorder.
XX
OS Synthetic.
OS Mastadenovirus.
XX
PN WO9807865-A1.
XX
PD 26-FEB-1998.
XX
PF 21-AUG-1997; 97WO-US14719.

XX
PR 21-AUG-1996; 96US-0701124.
XX
PA (GENV-) GENVEC INC.
XX
PI Kovesdi I, Roelvink PW, Wickham TJ;
XX
DR WPI; 1998-169169/15.
XX
PT Chimeric adenovirus fibre proteins - containing non-native amino
PT acid sequence to provide for binding and entry into cells,
PT especially for gene therapy
XX
PS Example 8; Page 57; 124pp; English.
XX
CC The present sequence represents an alpha4 integrins targeting sequence,
CC which is used in an example from the present invention. The present
CC invention describes a chimeric adenovirus fibre protein (AFP) containing
CC a constrained non-native amino acid sequence. The non-native amino acid
CC sequence allows the chimeric fibre (or a vector comprising the chimeric
CC fibre) to more efficiently bind to and enter cells. The products can be
CC used for gene therapy, for treating cancer, e.g. melanoma, glioma and
CC lung cancers as well as genetic disorders, e.g. cystic fibrosis,
CC haemophilia and muscular dystrophy as well as pathogenic infections,
CC e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g.
CC prevent restenosis following angioplasty or to promote angiogenesis to
CC reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's
CC disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 23; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 15
AAR11361
ID AAR11361 standard; peptide; 8 AA.
XX
AC AAR11361;
XX
DT 04-JUN-1991 (first entry)
XX
DE Peptide #352 derived from Cs-1 peptide of IIICS region.
XX
KW Fibronectin; extracellular matrix receptor; ECMR: type III;
KW connecting segment; IIICS; adhesion; alpha4beta1; lymphocyte;
KW autoimmune disease; allergy; asthma; ligand.
XX
OS Synthetic.
XX
PN WO9103252-A.
XX
PD 21-MAR-1991.
XX
PF 31-AUG-1990; 90WO-US04978.
XX
PR 01-SEP-1989; 89US-0402389.
XX
PA (WAYN/) WAYNER E.
XX
PI Wayner E;
XX
DR WPI; 1991-101865/14.
XX
PT Inhibition of lymphocyte adherence to vascular endothelium -
PT using a novel antibody or peptide for treatment of auto-immune
PT disease, asthma, allergy etc.
XX
PS Claim 10; Page 74; 92pp; English.
XX
CC The peptide is derived the CS-1 peptide (Humphries et al., 1987,
CC J. Biol. Chem. 262:6886-6892), from the IIICS variable region of
CC fibronectin. The peptide inhibits binding of lymphocytes to
CC endothelial cells preventing migration through the vascular
CC endothelium and into tissues. It acts by blocking the alpha4-
CC beta1 extracellular matrix receptor. Admin. of the peptide can
CC suppress the immune response and treat diseases associated with
CC chronic or relapsing activation of the immune system, including
CC collagen vascular diseases and other autoimmune diseases,
CC multiple sclerosis, asthma, allergy and chronic inflammatory skin
CC conditions.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

Search completed: June 10, 2002, 06:25:07
Job time: 232 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:36:37 ; Search time 14.32 Seconds
(without alignments)
33.551 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	43.5	4	2	A61300	22K superhelical D
2	10	43.5	5	2	PT0624	T-cell receptor be
3	8	34.8	4	2	I51049	metallothionein-A
4	8	34.8	4	2	E44823	synaptosomal-assoc
5	8	34.8	5	2	A32516	cholecystokinin-5
6	8	34.8	5	2	B31836	20K protein - Rick
7	7	30.4	4	2	A26209	protein-glutamine
8	7	30.4	5	2	S55237	zinc-binding prote
9	7	30.4	5	2	PT0278	Ig heavy chain CRD
10	6	26.1	4	2	I40697	biotin A - Citroba
11	6	26.1	4	2	A41890	protein D - Escher
12	6	26.1	4	2	D41654	hypothetical prote
13	6	26.1	4	2	A32480	achatin-I - giant
14	6	26.1	4	2	PT0271	Ig heavy chain CRD
15	6	26.1	4	2	B53284	T-cell receptor be
16	6	26.1	4	2	I54357	schwannomin - mous
17	6	26.1	4	2	PT0696	T-cell receptor be
18	6	26.1	4	2	PT0711	T-cell receptor be
19	6	26.1	5	2	A60521	glycogen phosphory
20	6	26.1	5	2	C23751	spinal cord peptid
21	6	26.1	5	2	A26830	mitosis inhibiting
22	6	26.1	5	2	B37325	pap fimbrial regul
23	6	26.1	5	2	A32014	traM protein - Esc
24	6	26.1	5	2	B60274	major protein anti
25	6	26.1	5	2	D60274	major protein anti
26	6	26.1	5	2	S70615	endo-1,4-beta-xyla
27	6	26.1	5	2	T14908	hypothetical prote
28	6	26.1	5	2	PQ0689	photosystem I 10.4
29	6	26.1	5	2	A44692	fulicin - giant Af
30	6	26.1	5	2	PT0267	Ig heavy chain CRD
31	6	26.1	5	2	PT0281	Ig heavy chain CRD
32	6	26.1	5	2	PT0308	Ig heavy chain CRD
33	6	26.1	5	2	PT0596	T-cell receptor be
34	6	26.1	5	2	PT0513	T-cell receptor be
35	6	26.1	5	2	PT0600	T-cell receptor be
36	6	26.1	5	2	PT0729	T-cell receptor be
37	6	26.1	5	2	PT0601	T-cell receptor be
38	6	26.1	5	2	PT0672	T-cell receptor be
39	6	26.1	5	2	PT0660	T-cell receptor be
40	6	26.1	5	2	PT0651	T-cell receptor be
41	6	26.1	5	2	PT0656	T-cell receptor be
42	6	26.1	5	2	PT0535	T-cell receptor be
43	6	26.1	5	2	PT0699	T-cell receptor be
44	6	26.1	5	2	PT0538	T-cell receptor be
45	6	26.1	5	2	PT0561	T-cell receptor be
46	6	26.1	5	2	PT0540	T-cell receptor be
47	6	26.1	5	2	PT0703	T-cell receptor be
48	6	26.1	5	2	PT0690	T-cell receptor be
49	6	26.1	5	2	PT0573	T-cell receptor be
50	6	26.1	5	2	PT0580	T-cell receptor be
51	6	26.1	5	2	PT0679	T-cell receptor be
52	6	26.1	5	2	S68326	blood cell protein
53	6	26.1	5	2	S69237	surface protein te
54	5	21.7	3	3	A33802	thyrotropin-releas
55	5	21.7	4	2	A37832	phenol 2-monooxyge
56	5	21.7	4	2	I57745	D-mannonate hydrol
57	5	21.7	4	2	B43848	cell surface adhes
58	5	21.7	4	2	I40505	hypothetical prote
59	5	21.7	4	2	I40804	endoglucanase F -
60	5	21.7	4	2	A27897	glucan 1,4-alpha-g
61	5	21.7	4	2	PT0677	T-cell receptor be
62	5	21.7	4	2	S55238	pallidipin - assas
63	5	21.7	5	2	JN0862	peptidyl-dipeptida
64	5	21.7	5	2	B41225	copper resistance
65	5	21.7	5	2	B22565	R-phycoerythrin al
66	5	21.7	5	2	T14910	hypothetical prote
67	5	21.7	5	2	A33882	cadmium-binding pe
68	5	21.7	5	2	B37988	acid proteinase li
69	5	21.7	5	2	B45525	actin I - malaria
70	5	21.7	5	2	B61168	cocoonase (EC 3.4.
71	5	21.7	5	2	JT0520	Ig kappa chain V-I
72	5	21.7	5	2	B44823	synaptosomal-assoc
73	5	21.7	5	2	D44823	synaptosomal-assoc
74	5	21.7	5	2	PT0610	T-cell receptor be
75	5	21.7	5	2	PT0684	T-cell receptor be
76	4	17.4	3	3	PQ0010	angiotensin-conver
77	4	17.4	3	3	T13892	cytochrome-c oxida
78	4	17.4	4	2	S18401	thyroglobulin - do
79	4	17.4	4	2	A32039	tyrosine-melanocyt
80	4	17.4	4	2	A48360	gamma subunit of P
81	4	17.4	4	2	T46627	hypothetical prote
82	4	17.4	4	2	S09478	globulin IV alpha
83	4	17.4	4	2	S17255	ribosomal protein
84	4	17.4	4	2	T30569	hypothetical prote
85	4	17.4	4	2	I38888	COI intron 16 prot
86	4	17.4	4	2	A35779	neuropeptide Antho
87	4	17.4	4	2	PT0240	Ig heavy chain CRD
88	4	17.4	4	2	A53284	T-cell receptor be
89	4	17.4	4	2	PT0645	T-cell receptor be
90	4	17.4	4	2	PT0633	T-cell receptor be
91	4	17.4	4	2	PT0551	T-cell receptor be
92	4	17.4	4	2	PT0697	T-cell receptor be
93	4	17.4	4	2	PT0721	T-cell receptor be
94	4	17.4	4	2	A40135	branched-chain-ami
95	4	17.4	4	2	S47552	ubiquitin - rat
96	4	17.4	5	1	HOROHA	proctolin - Americ
97	4	17.4	5	2	JN0860	peptidyl-dipeptida
98	4	17.4	5	2	C41225	copper resistance
99	4	17.4	5	2	I40702	primase - Citrobac
100	4	17.4	5	2	E42364	flagellar protein

ALIGNMENTS

RESULT 1
A61300
22K superhelical DNA-binding protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: A61300
R;Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
J. Biochem. 92, 1059-1068, 1982
A;Title: Purification and characterization of a protein from Escherichia coli which form
A;Reference number: A61300; MUID:83082696
A;Accession: A61300
A;Molecule type: protein
A;Residues: 1-4 <KIS>
C;Comment: This protein resembles some of the histone-like protein of bacteria in amino
C;Keywords: DNA binding; monomer

Query Match 43.5%; Score 10; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eil 3
||:
Db 2 EIV 4

RESULT 2
PT0624
T-cell receptor beta chain V-D-J region (120-1K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0624
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0624
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 43.5%; Score 10; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ld 4
||
Db 4 LD 5

RESULT 3
I51049
metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) me
A;Reference number: I51049; MUID:95324545
A;Accession: I51049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <OLS>
A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 34.8%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ld 4
:|
Db 1 MD 2

RESULT 4
E44823
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N;Alternate names: superprotein peptide 1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: E44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein)
A;Reference number: A44823; MUID:92044785
A;Accession: E44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <LOE>
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)
C;Keywords: membrane trafficking

Query Match 34.8%; Score 8; DB 2; Length 4;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ild 4
|::
Db 1 IME 3

RESULT 5
A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A;Reference number: A32516; MUID:87153871
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.8%; Score 8; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ld 4
:|
Db 3 MD 4

RESULT 6
B31836
20K protein - Rickettsia rickettsii (fragment)
C;Species: Rickettsia rickettsii
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C;Accession: B31836

R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia ricke
A;Reference number: A91885; MUID:89008059
A;Accession: B31836
A;Molecule type: DNA
A;Residues: 1-5 <AND>
A;Cross-references: GB:J03371; NID:g152455; PIDN:AAD15030.1; PID:g4262874

Query Match 34.8%; Score 8; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      3 ld 4
          :|
Db      1 MD 2
```

RESULT 7
A26209
protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 10-Sep-1987 #sequence_revision 10-Sep-1987 #text_change 03-Mar-1995
C;Accession: A26209
R;Connellan, J.M.; Chung, S.I.; Whetzel, N.K.; Bradley, L.M.; Folk, J.E.
J. Biol. Chem. 246, 1093-1098, 1971
A;Title: Structural properties of guinea pig liver transglutaminase.
A;Reference number: A26209; MUID:71111415
A;Accession: A26209
A;Molecule type: protein
A;Residues: 1-4 <CON>
A;Experimental source: liver
C;Keywords: aminoacyltransferase

Query Match 30.4%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      4 dv 5
          |:
Db      3 DL 4
```

RESULT 8
S55237
zinc-binding protein ZBP14 - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S55237
R;Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995
A;Title: Expression and characterization of maize ZBP14, a member of a new family of zin
A;Reference number: S55237; MUID:95234046
A;Accession: S55237
A;Molecule type: protein
A;Residues: 1-5 <ROB>

Query Match 30.4%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 il 3
          :|
Db      4 VL 5
```

RESULT 9
PT0278
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0278
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0278
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.4%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 il 3
          :|
Db      4 VL 5
```

RESULT 10
I40697
biotin A - Citrobacter freundii (fragment)
C;Species: Citrobacter freundii
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C;Accession: I40697
R;Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A;Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citroba
A;Reference number: I40697; MUID:89006280
A;Accession: I40697
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <RES>
A;Cross-references: GB:M21922; NID:g144434

Query Match 26.1%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      4 d 4
          |
Db      3 D 3
```

RESULT 11
A41890
protein D - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: A41890
R;Slettan, A.; Gebhardt, K.; Kristiansen, E.; Birkeland, N.K.; Lindqvist, B.H.
J. Bacteriol. 174, 4094-4100, 1992
A;Title: Escherichia coli K-12 and B contain functional bacteriophage P2 ogr genes.
A;Reference number: A41890; MUID:92283767
A;Accession: A41890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <SLE>
A;Cross-references: GB:M81463

Query Match 26.1%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      4 d 4
          |
Db      2 D 2
```

```
RESULT  12
D41654
hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)
C;Species: Haemophilus parainfluenzae
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995
C;Accession: D41654
R;Kroll, J.S.; Langford, P.R.; Loynds, B.M.
J. Bacteriol. 173, 7449-7457, 1991
A;Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus para
A;Reference number: A41654; MUID:92041655
A;Accession: D41654
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <KRO>


  Query Match             26.1%;  Score 6;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      1 D 1


RESULT  13
A32480
achatin-I - giant African snail
N;Contains: achatin-II
C;Species: Achatina fulica (giant African snail)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
C;Accession: A32480
R;Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun
Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru
A;Reference number: A32480; MUID:89273551
A;Accession: A32480
A;Molecule type: protein
A;Residues: 1-4 <KAM>
A;Note: stereochemistry of the active form confirmed by chemical synthesis
R;Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto
FEBS Lett. 307, 253-256, 1992
A;Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro
(H-Gly-Phe-Ala-Asp-OH).
A;Reference number: A44691; MUID:92354723
A;Contents: annotation; X-ray crystallography, 0.85 angstroms
A;Note: achatin-II has L-phenylalanine
C;Keywords: D-amino acid
F;2/Modified site: D-phenylalanine (Phe) #status experimental


  Query Match             26.1%;  Score 6;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4


RESULT  14
PT0271
Ig heavy chain CRD3 region (clone 3-103A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0271
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0271
A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin


  Query Match             26.1%;  Score 6;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      1 D 1


RESULT  15
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity an
A;Reference number: A53284; MUID:91342695
A;Accession: B53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19518.1; PID:g233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor


  Query Match             26.1%;  Score 6;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      1 D 1


RESULT  16
I54357
schwannomin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I54357
R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are
A;Reference number: I54357; MUID:95072570
A;Accession: I54357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4 <RES>
A;Cross-references: GB:L28838; NID:g454836; PIDN:AAA57150.1; PID:g601923
C;Genetics:
A;Gene: NF2


  Query Match             26.1%;  Score 6;  DB 2;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ei 2
          |:
Db      3 EM 4


RESULT  17
PT0696
T-cell receptor beta chain V-D-J region (100-2N) - mouse (fragment)
```

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0635; PT0612; PT0545; PT0692; PT0552; PT0696
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0635
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, 100-2N
A;Accession: PT0612
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, 111-1J
A;Accession: PT0545
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AD
A;Accession: PT0692
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE4>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1M
A;Accession: PT0552
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE5>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 126-1CI
A;Accession: PT0696
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE6>
A;Experimental source: newborn thymus, strain BALB/c, 135-1AA
C;Keywords: T-cell receptor

```
  Query Match             26.1%;  Score 6;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4
```

RESULT 18
PT0711
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0607
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE1>
A;Experimental source: newborn thymus, strain BALB/c, 120-2J
A;Accession: PT0674
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A;Accession: PT0678
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A;Accession: PT0570
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE4>
A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A;Accession: PT0711
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE5>
A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C;Keywords: T-cell receptor

```
  Query Match             26.1%;  Score 6;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4
```

RESULT 19
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal
A;Reference number: A60521; MUID:90227907
A;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Superfamily: phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status expe

```
  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ei 2
          :|
Db      1 QI 2
```

RESULT 20
C23751
spinal cord peptide SCP-6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C;Accession: C23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425
A;Accession: C23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <HSI>
C;Superfamily: unassigned animal peptides

```
  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
```

```
Db      1 D 1


RESULT  21
A26830
mitosis inhibiting peptide - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: A26830
R;Reichelt, K.; Elgjo, K.; Edminson, P.D.
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
A;Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
A;Reference number: A26830; MUID:87298602
A;Accession: A26830
A;Molecule type: protein
A;Residues: 1-5 <REI>
C;Superfamily: unassigned animal peptides
C;Keywords: blocked amino end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      3 D 3


RESULT  22
B37325
pap fimbrial regulatory protein papI - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
C;Accession: B37325
R;Braaten, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.
J. Bacteriol. 173, 1789-1800, 1991
A;Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex
A;Reference number: A37325; MUID:91154136
A;Accession: B37325
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <BRA>
A;Cross-references: GB:M63747


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   33.3%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 eil 3
          | :
Db      3 EYM 5


RESULT  23
A32014
traM protein - Escherichia coli plasmid R100 (fragment)
C;Species: Escherichia coli
C;Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 16-Feb-1997
C;Accession: A32014
R;Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A;Title: Identification and characterization of the products from the traJ and traY gene
A;Reference number: A32014; MUID:88227859
A;Accession: A32014
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <INA>
C;Genetics:
A;Genome: plasmid
C;Keywords: DNA binding


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      3 D 3


RESULT  24
B60274
major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: B60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the cult
A;Reference number: A60274; MUID:91099989
A;Accession: B60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      1 D 1


RESULT  25
D60274
major protein antigen MPT46 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: D60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the cult
A;Reference number: A60274; MUID:91099989
A;Accession: D60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      2 D 2


RESULT  26
S70615
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (frag
N;Alternate names: xylanase
C;Species: Streptomyces sp.
A;Variety: Chainia sp. NCL 82.5.1
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C;Accession: S70615
R;Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
Biochem. J. 316, 771-775, 1996
A;Title: Structural environment of an essential cysteine residue of xylanase from Cha
A;Reference number: S70615; MUID:96265041
```

A;Accession: S70615
A;Molecule type: protein
A;Residues: 1-5 <RAO>
A;Experimental source: Chainia sp. strain NCL 82.5.1
A;Note: the source is designated as Chainia sp.
C;Function:
A;Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
A;Pathway: fermentation of hemicellulose into ethanol
C;Keywords: glycosidase; hydrolase

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 d 4
|
Db 5 D 5

RESULT 27
T14908
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14908
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918
A;Accession: T14908
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5 <KIR>
A;Cross-references: EMBL:Y10809; NID:g3336901; PIDN:CAA71767.1; PID:g3336902
A;Experimental source: Hamburger Schnitt

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ildv 5
:: |
Db 1 MVSV 4

RESULT 28
PQ0689
photosystem I 10.4K H1 chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0689
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are a
A;Reference number: PQ0667; MUID:94105345
A;Accession: PQ0689
A;Molecule type: protein
A;Residues: 1-5 <OBO>
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 d 4
|
Db 4 D 4

RESULT 29
A44692
fulicin - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C;Accession: A44692
R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.;
Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated fro
A;Reference number: A44692; MUID:91315471
A;Accession: A44692
A;Molecule type: protein
A;Residues: 1-5 <OHT>
C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F;2/Modified site: D-asparagine (Asn) #status experimental
F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 eil 3
| :
Db 3 EFV 5

RESULT 30
PT0267
Ig heavy chain CRD3 region (clone 3-94A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0267
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0267
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 d 4
|
Db 5 D 5

RESULT 31
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0281
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      4 d 4
          |
Db      1 D 1


RESULT  32
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0308
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337
A;Accession: PT0308
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      1 D 1


RESULT  33
PT0596
T-cell receptor beta chain V-D-J region (100-2AE) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0596; PT0614
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0596
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AE
A;Accession: PT0614
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1H
C;Keywords: T-cell receptor


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4


RESULT  34
PT0513
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0513; PT0606
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0513
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AL
A;Accession: PT0606
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1S
C;Keywords: T-cell receptor


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4


RESULT  35
PT0600
T-cell receptor beta chain V-D-J region (120-1C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0600
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0600
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4



Search completed: June 10, 2002, 06:37:52
Job time: 75 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:37:57 ; Search time 11.71 Seconds
(without alignments)
16.533 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	34.8	3	1	LUXE_VIBFI	P24272 vibrio fisc
2	8	34.8	5	1	UC22_MAIZE	P80628 zea mays (m
3	7	30.4	5	1	RE11_LITRU	P82070 litoria rub
4	6	26.1	4	1	ACH1_ACHFU	P35904 achatina fu
5	6	26.1	4	1	OCP1_OCTMI	P58648 octopus min
6	6	26.1	4	1	OCP3_OCTMI	P58649 octopus min
7	6	26.1	5	1	BIOA_CITFR	P13071 citrobacter
8	6	26.1	5	1	TRM3_ECOLI	P13973 escherichia
9	6	26.1	5	1	UXA4_CHLTR	P38005 chlamydia t
10	5	21.7	4	1	EOSI_HUMAN	P02731 homo sapien
11	5	21.7	5	1	EI04_LITRU	P82100 litoria rub
12	5	21.7	5	1	RE21_LITRU	P82071 litoria rub
13	5	21.7	5	1	RE31_LITRU	P82072 litoria rub
14	4	17.4	4	1	FAR3_HIRME	P42562 hirudo medi
15	4	17.4	4	1	FLRF_HIRME	P42561 hirudo medi
16	4	17.4	4	1	FLRN_ANTEL	P58707 anthopleura
17	4	17.4	4	1	FYRI_ANTEL	P58706 anthopleura
18	4	17.4	4	1	RM01_YEAST	P36515 saccharomyc
19	4	17.4	5	1	AL14_CARMA	P81817 carcinus ma
20	4	17.4	5	1	EI03_LITRU	P82099 litoria rub
21	4	17.4	5	1	FARP_ARTTR	P41853 artioposthi
22	4	17.4	5	1	PRCT_PERAM	P01373 periplaneta
23	4	17.4	5	1	PSK_DAUCA	P58261 daucus caro
24	4	17.4	5	1	RE32_LITRU	P82073 litoria rub
25	4	17.4	5	1	TPIS_CANFA	P54714 canis famil
26	4	17.4	5	1	UF01_MOUSE	P38639 mus musculu
27	2	8.7	3	1	THYL_PIG	P01151 sus scrofa
28	2	8.7	4	1	DCML_PSECH	P19916 pseudomonas
29	2	8.7	4	1	DCMS_PSECH	P19918 pseudomonas
30	2	8.7	4	1	FAR4_HIRME	P42563 hirudo medi
31	2	8.7	4	1	FMRF_MACNI	P01162 macrocallis
32	2	8.7	5	1	BIOB_CITFR	P12997 citrobacter
33	2	8.7	5	1	BPP7_BOTIN	P30425 bothrops in
34	1	4.3	3	1	GRWM_HUMAN	P01157 homo sapien
35	1	4.3	4	1	FFKA_ANTEL	P58705 anthopleura
36	1	4.3	4	1	TUFT_HUMAN	P01858 homo sapien
37	0	0.0	5	1	PAP2_PARMA	P81864 pardachirus
38	0	0.0	5	1	SUGA_ACHDO	P19991 acheta dome

ALIGNMENTS

RESULT 1
LUXE_VIBFI
ID LUXE_VIBFI STANDARD; PRT; 3 AA.
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
GN LUXE.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon.";
RL J. Bacteriol. 172:6797-6802(1990).
CC -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC an acyl-protein thiolester.
CC -!- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
CC COMPLEX.
CC ---

CC ---
DR EMBL; M62812; -; NOT_ANNOTATED_CDS.
KW Luminescence; Ligase.
FT NON_TER 1 1
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 34.8%; Score 8; DB 1; Length 3;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ild 4
| |
Db 1 IKD 3

RESULT 2
UC22_MAIZE
ID UC22_MAIZE STANDARD; PRT; 5 AA.
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Coleoptile;
RA   Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA   Pernollet J.-C., Zivy M., de Vienne D.;
RT   "The maize two dimensional gel protein database: towards an integrated
RT   genome analysis program.";
RL   Theor. Appl. Genet. 93:997-1005(1996).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
DR   Maize-2DPAGE; P80628; COLEOPTILE.
DR   MaizeDB; 123954; -.
FT   NON_TER       1      1
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  654 MW;  72CB19C9C0300000 CRC64;


  Query Match             34.8%;  Score 8;  DB 1;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ei 2
          |:
Db      4 EV 5


RESULT   3
RE11_LITRU
ID   RE11_LITRU     STANDARD;      PRT;      5 AA.
AC   P82070;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 1.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  598 MW;  6DD9C9CAB2A00000 CRC64;


  Query Match             30.4%;  Score 7;  DB 1;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 ld 4
          :|
Db      1 VD 2


RESULT   4
ACH1_ACHFU
ID   ACH1_ACHFU     STANDARD;      PRT;      4 AA.
AC   P35904;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Achatin-I.
OS   Achatina fulica (Giant African snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Achatinacea; Achatinidae; Achatina.
OX   NCBI_TaxID=6530;
RN   [1]
RP   SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC   STRAIN=FERUSSAC; TISSUE=Ganglion;
RX   MEDLINE=89273551; PubMed=2597281;
RA   Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA   Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA   Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT   "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT   fulica Ferussac containing a D-amino acid residue.";
RL   Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN   [2]
RP   CHARACTERIZATION.
RC   STRAIN=FERUSSAC; TISSUE=Heart atrium;
RX   MEDLINE=91264856; PubMed=1675568;
RA   Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA   Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT   "Purification of achatin-I from the atria of the African giant snail,
RT   Achatina fulica, and its possible function.";
RL   Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=93014529; PubMed=1399265;
RA   Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA   Iwashita T., Nomoto K.;
RT   "Crystal structure and molecular conformation of achatin-I
RT   (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT   D-amino acid residue.";
RL   Int. J. Pept. Protein Res. 39:258-264(1992).
CC   -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC       AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC       NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC       HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR   PIR; A32480; A32480.
KW   Hormone; D-amino acid.
FT   MOD_RES       2      2       D-PHENYLALANINE.
SQ   SEQUENCE   4 AA;  408 MW;  6AADD9C810000000 CRC64;


  Query Match             26.1%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4


RESULT   5
OCP1_OCTMI
ID   OCP1_OCTMI     STANDARD;      PRT;      4 AA.
AC   P58648;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cardioactive peptides Ocp-1/Ocp-2.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC   Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=89766;
RN   [1]
RP   SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   PubMed=10876044;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
```

```
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC       inotropic effects on the heart. Ocp-2 is a 1000 time less
CC       active than Ocp-1.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-PHENYLALANINE.
SQ   SEQUENCE   4 AA;  394 MW;  6AA879C810000000 CRC64;


  Query Match             26.1%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4


RESULT   6
OCP3_OCTMI
ID   OCP3_OCTMI     STANDARD;      PRT;     4 AA.
AC   P58649;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cardioactive peptides Ocp-3/Ocp-4.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC   Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=89766;
RN   [1]
RP   SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   PubMed=10876044;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC       inotropic effects on the heart. Ocp-4 is a 1000 time less
CC       active than Ocp-3.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-SERINE (IN OCP-4).
SQ   SEQUENCE   4 AA;  463 MW;  6AB365B810000000 CRC64;


  Query Match             26.1%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4


RESULT   7
BIOA_CITFR
ID   BIOA_CITFR     STANDARD;      PRT;     5 AA.
AC   P13071;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE   (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE   aminotransferase) (Fragment).
GN   BIOA.
OS   Citrobacter freundii.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Citrobacter.
OX   NCBI_TaxID=546;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89006280; PubMed=2971595;
RA   Shiuan D., Campbell A.;
RT   "Transcriptional regulation and gene arrangement of Escherichia coli,
RT   Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL   Gene 67:203-211(1988).
CC   -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC       oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC       diaminononanoate.
CC   -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC   -!- PATHWAY: BIOTIN BIOSYNTHESIS.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC       AMINOTRANSFERASES.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR   InterPro; IPR000954; Aminotran_3.
DR   PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW   Biotin biosynthesis; Transferase; Aminotransferase;
KW   Pyridoxal phosphate.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  582 MW;  6AAAB1B1A6F00000 CRC64;


  Query Match             26.1%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4


RESULT   8
TRM3_ECOLI
ID   TRM3_ECOLI     STANDARD;      PRT;     5 AA.
AC   P13973;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   TraM protein (Fragment).
GN   TRAM.
OS   Escherichia coli.
OG   Plasmid IncFII R100.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88227859; PubMed=2836369;
RA   Inamoto S., Yoshioka Y., Ohtsubo E.;
RT   "Identification and characterization of the products from the traJ
RT   and traY genes of plasmid R100.";
RL   J. Bacteriol. 170:2749-2757(1988).
CC   -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC       PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M20941; -; NOT_ANNOTATED_CDS.
DR   PIR; A32014; A32014.
KW   Conjugation; Plasmid; DNA-binding.
FT   NON_TER       1      1
SQ   SEQUENCE   5 AA;  634 MW;  6B1B1AA443500000 CRC64;


  Query Match             26.1%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      3 D 3


RESULT   9
UXA4_CHLTR
ID   UXA4_CHLTR     STANDARD;      PRT;     5 AA.
AC   P38005;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Unknown protein from 2D-page from elementary body (Fragment).
OS   Chlamydia trachomatis.
OC   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX   NCBI_TaxID=813;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=L2/434/BU;
RA   Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA   Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
RA   Pallini V.;
RL   Submitted (SEP-1994) to the SWISS-PROT data bank.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
DR   Siena-2DPAGE; P38005; -.
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  474 MW;  75BAA865AA800000 CRC64;


  Query Match             26.1%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      4 D 4


RESULT  10
EOSI_HUMAN
ID   EOSI_HUMAN     STANDARD;      PRT;     4 AA.
AC   P02731;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   Eosinophilotactic peptides.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76078412; PubMed=1060093;
RA   Goetzl E.J., Austen K.F.;
RT   "Purification and synthesis of eosinophilotactic tetrapeptides of
RT   human lung tissue: identification as eosinophil chemotactic factor of
RT   anaphylaxis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC   -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC       (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC       (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC       EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC       OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR   PIR; A03190; ETHUL.
FT   VARIANT       1      1       V -> A (IN OTHER PEPTIDE).
FT                                /FTId=VAR_005201.
SQ   SEQUENCE   4 AA;  390 MW;  6B05B862A0000000 CRC64;


  Query Match             21.7%;  Score 5;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          |
Db      4 E 4


RESULT  11
EI04_LITRU
ID   EI04_LITRU     STANDARD;      PRT;     5 AA.
AC   P82100;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Electrin 4.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
CC   -!- SUBCELLULAR LOCATION: SECRETED.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5      5       AMIDATION.
SQ   SEQUENCE   5 AA;  616 MW;  61F2D1A059A00000 CRC64;


  Query Match             21.7%;  Score 5;  DB 1;  Length 5;
  Best Local Similarity   33.3%;  Pred. No. 1e+05;
  Matches    1;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 ldv 5
          : |
Db      2 ITV 4


RESULT  12
RE21_LITRU
ID   RE21_LITRU     STANDARD;      PRT;     5 AA.
AC   P82071;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
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RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  626 MW;  6DD9C9CB10300000 CRC64;


  Query Match             21.7%;  Score 5;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          |
Db      2 E 2


RESULT  13
RE31_LITRU
ID   RE31_LITRU     STANDARD;      PRT;     5 AA.
AC   P82072;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 3.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  656 MW;  71A9C9CB10300000 CRC64;


  Query Match             21.7%;  Score 5;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          |
Db      2 E 2


RESULT  14
FAR3_HIRME
ID   FAR3_HIRME     STANDARD;      PRT;     4 AA.
AC   P42562;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFamide-like neuropeptide YLRF-amide.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  598 MW;  69D4073B30000000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          |
Db      2 L 2


RESULT  15
FLRF_HIRME
ID   FLRF_HIRME     STANDARD;      PRT;     4 AA.
AC   P42561;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FLRFamide.
OS   Hirudo medicinalis (Medicinal leech), and
OS   Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421, 27815;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=H.medicinalis;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=H.trivolvis; TISSUE=Kidney;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  582 MW;  69D40729A0000000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          |
Db      2 L 2


RESULT  16
FLRN_ANTEL
ID   FLRN_ANTEL     STANDARD;      PRT;     4 AA.
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AC   P58707;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Antho-RNamide.
OS   Anthopleura elegantissima (Sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE, AND MASS-SPECTROMETRY.
RX   PubMed=1973541;
RA   Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA   Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT   "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT   anemone neuropeptide containing an unusual amino-terminal blocking
RT   group.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron-specific.
CC   -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       L-3-PHENYLLACTYL.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  549 MW;  64540729A0000000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          |
Db      2 L 2


RESULT  17
FYRI_ANTEL
ID   FYRI_ANTEL     STANDARD;      PRT;     4 AA.
AC   P58706;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Antho-RIamide I [Contains: Antho-RIamide II].
OS   Anthopleura elegantissima (Sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE.
RX   PubMed=1821096;
RA   Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA   Grimmelikhuijzen C.J.P.;
RT   "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT   biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its
RT   des-phenyllactyl fragment Tyr-Arg-Ile-NH2.";
RL   Peptides 12:1165-1173(1991).
RN   [2]
RP   FUNCTION.
RX   PubMed=8397415;
RA   McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT   "The expansion behaviour of sea anemones may be coordinated by two
RT   inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC   -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC       groups. May be involved in the expansion phase of feeding
CC       behaviour in sea anemones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron-specific.
KW   Neuropeptide; Amidation.
FT   CHAIN         1      4       ANTHO-RIAMIDE I.
FT   CHAIN         2      4       ANTHO-RIAMIDE II.
FT   MOD_RES       1      1       L-3-PHENYLLACTYL.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  598 MW;  60441B59A0000000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 i 2
          |
Db      4 I 4


RESULT  18
RM01_YEAST
ID   RM01_YEAST     STANDARD;      PRT;     4 AA.
AC   P36515;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN   MRPL1.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91285106; PubMed=2060626;
RA   Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA   Kitakawa M.;
RT   "Extended N-terminal sequencing of proteins of the large ribosomal
RT   subunit from yeast mitochondria.";
RL   FEBS Lett. 284:51-56(1991).
DR   PIR; S17255; S17255.
DR   SGD; L0002681; MRPL1.
KW   Ribosomal protein; Mitochondrion.
FT   NON_TER       4      4
SQ   SEQUENCE   4 AA;  402 MW;  7771B2D5D0000000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 v 5
          |
Db      2 V 2


RESULT  19
AL14_CARMA
ID   AL14_CARMA     STANDARD;      PRT;     5 AA.
AC   P81817;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 14.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
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CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       5      5       AMIDATION (POTENTIAL).
SQ   SEQUENCE   5 AA;  586 MW;  672879D5AB300000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          |
Db      5 L 5


RESULT  20
EI03_LITRU
ID   EI03_LITRU     STANDARD;      PRT;     5 AA.
AC   P82099;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Electrin 3.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
CC   -!- SUBCELLULAR LOCATION: SECRETED.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5      5       AMIDATION.
SQ   SEQUENCE   5 AA;  630 MW;  668761F2C9A00000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 v 5
          |
Db      2 V 2


RESULT  21
FARP_ARTTR
ID   FARP_ARTTR     STANDARD;      PRT;     5 AA.
AC   P41853;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFamide-like neuropeptide RYIRF-amide.
OS   Artioposthia triangulata.
OC   Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC   Rhabditophora; Seriata; Tricladida; Terricola; Geoplanidae;
OC   Arthurdendyus.
OX   NCBI_TaxID=132421;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RX   MEDLINE=94211927; PubMed=7909164;
RA   Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT   "RYIRFamide: a turbellarian FMRFamide-related peptide (FaRP).";
RL   Regul. Pept. 50:37-43(1994).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       5      5       AMIDATION.
SQ   SEQUENCE   5 AA;  754 MW;  69D4004B44600000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 i 2
          |
Db      3 I 3


RESULT  22
PRCT_PERAM
ID   PRCT_PERAM     STANDARD;      PRT;     5 AA.
AC   P01373;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Proctolin.
OS   Periplaneta americana (American cockroach),
OS   Limulus polyphemus (Atlantic horseshoe crab), and
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blattoidea; Blattidae; Periplaneta.
OX   NCBI_TaxID=6978, 6850, 6759;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=76074708; PubMed=576;
RA   Starratt A.N., Brown B.E.;
RT   "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT   in insects.";
RL   Life Sci. 17:1253-1256(1975).
RN   [2]
RP   BIOLOGICAL SOURCE.
RC   SPECIES=P.americana;
RX   MEDLINE=81225865; PubMed=6113690;
RA   O'Shea M., Adams M.E.;
RT   "Pentapeptide (proctolin) associated with an identified neuron.";
RL   Science 213:567-569(1981).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=L.polyphemus;
RX   MEDLINE=90287800; PubMed=2356151;
RA   Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA   Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA   Shabanowitz J.;
RT   "Identification of proctolin in the central nervous system of the
RT   horseshoe crab, Limulus polyphemus.";
RL   Peptides 11:205-211(1990).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=C.maenas;
RX   MEDLINE=86232789; PubMed=2872661;
RA   Stangier J., Dircksen H., Keller R.;
RT   "Identification and immunocytochemical localization of proctolin in
RT   pericardial organs of the shore crab, Carcinus maenas.";
RL   Peptides 7:67-72(1986).
CC   -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC       MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC   -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC       THE CRAB PERICARDIAL ORGANS.
DR   PIR; A01644; HOROHA.
DR   PIR; A60411; A60411.
KW   Neuropeptide.
SQ   SEQUENCE   5 AA;  649 MW;  71B7673B44600000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
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  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          |
Db      3 L 3


RESULT  23
PSK_DAUCA
ID   PSK_DAUCA      STANDARD;      PRT;     5 AA.
AC   P58261;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-
DE   beta)].
OS   Daucus carota (Carrot).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX   NCBI_TaxID=4039;
RN   [1]
RP   SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC   STRAIN=cv. US-Harumakigosun;
RX   MEDLINE=20212743; PubMed=10750705;
RA   Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA   Kamada H., Sakagami Y.;
RT   "A secreted peptide growth factor, phytosulfokine, acting as a
RT   stimulatory factor of carrot somatic embryo formation.";
RL   Plant Cell Physiol. 41:27-32(2000).
CC   -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC       CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC       EMBRYOS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC       PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW   Growth factor; Sulfation.
FT   PEPTIDE       1      4       PHYTOSULFOKINE-BETA.
FT   MOD_RES       1      1       SULFATION.
FT   MOD_RES       3      3       SULFATION.
SQ   SEQUENCE   5 AA;  687 MW;  76C1BB504B300000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 i 2
          |
Db      2 I 2


RESULT  24
RE32_LITRU
ID   RE32_LITRU     STANDARD;      PRT;     5 AA.
AC   P82073;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 3.2.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  570 MW;  71A9C9C862A00000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 v 5
          |
Db      1 V 1


RESULT  25
TPIS_CANFA
ID   TPIS_CANFA     STANDARD;      PRT;     5 AA.
AC   P54714;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN   TPI1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=98163340; PubMed=9504812;
RA   Dunn M.J., Corbett J.M., Wheeler C.H.;
RT   "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT   dog heart proteins.";
RL   Electrophoresis 18:2795-2802(1997).
CC   -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC       phosphate.
CC   -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR   HSC-2DPAGE; P54714; DOG.
DR   InterPro; IPR000652; Trioseph_isomerase.
DR   PROSITE; PS00171; TIM; PARTIAL.
KW   Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW   Pentose shunt.
FT   NON_TER       1      1
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  550 MW;  64444862C9A00000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 v 5
          |
Db      2 V 2


RESULT  26
UF01_MOUSE
ID   UF01_MOUSE     STANDARD;      PRT;     5 AA.
AC   P38639;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95009907; PubMed=7523108;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT   "Separation and sequencing of familiar and novel murine proteins
RT   using preparative two-dimensional gel electrophoresis.";
RL   Electrophoresis 15:735-745(1994).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  717 MW;  7364087043100000 CRC64;


  Query Match             17.4%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 i 2
          |
Db      2 I 2


RESULT  27
THYL_PIG
ID   THYL_PIG       STANDARD;      PRT;     3 AA.
AC   P01151;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
OS   Sus scrofa (Pig),
OS   Ovis aries (Sheep),
OS   Bombina orientalis (Oriental fire-bellied toad), and
OS   Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823, 9940, 8346, 8316;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=Pig; TISSUE=Hypothalamus;
RX   MEDLINE=70136150; PubMed=4984938;
RA   Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT   "Structure of porcine thyrotropin releasing hormone.";
RL   Biochemistry 9:1103-1106(1970).
RN   [2]
RP   SYNTHESIS.
RC   SPECIES=Pig;
RX   MEDLINE=70039904; PubMed=4982117;
RA   Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
RT   "The identity of chemical and hormonal properties of the thyrotropin
RT   releasing hormone and pyroglutamyl-histidyl-proline amide.";
RL   Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=Sheep; TISSUE=Hypothalamus;
RA   Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
RA   Ward D.N.;
RT   "The elucidation of the primary structure of the hypothalamic thyroid
RT   stimulating hormone releasing factor of ovine origin by means of mass
RT   spectrometry.";
RL   Org. Mass Spectrom. 5:221-228(1971).
RN   [4]
RP   SYNTHESIS.
RC   SPECIES=Sheep;
RX   MEDLINE=70163386; PubMed=4985794;
RA   Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
RA   Guillemin R.;
RT   "Characterization of ovine hypothalamic hypophysiotropic
RT   TSH-releasing factor.";
RL   Nature 226:321-325(1970).
RN   [5]
RP   SEQUENCE.
RC   SPECIES=B.orientalis; TISSUE=Skin;
RX   MEDLINE=76138399; PubMed=815011;
RA   Yasuhara T., Nakajima T.;
RT   "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
RL   Chem. Pharm. Bull. 23:3301-3303(1975).
RN   [6]
RP   SEQUENCE.
RC   SPECIES=N.viridescens;
RX   MEDLINE=75035605; PubMed=4214528;
RA   Grimm-Joergensen Y., McKelvy J.F.;
RT   "Biosynthesis of thyrotropin releasing factor by newt (Triturus
RT   viridescens) brain in vitro. Isolation and characterization of
RT   thyrotropin releasing factor.";
RL   J. Neurochem. 23:471-478(1974).
CC   -!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
CC       IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
CC       NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
DR   PIR; A01415; RHPGT.
DR   PIR; A93750; RHSHT.
DR   PIR; A90919; RHTDTO.
DR   PIR; A92971; A92971.
KW   Amidation.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       3       3       AMIDATION.
SQ   SEQUENCE   3 AA;  380 MW;  7761F6B0000000000 CRC64;


  Query Match             8.7%;  Score 2;  DB 1;  Length 3;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          :
Db      1 Q 1


RESULT  28
DCML_PSECH
ID   DCML_PSECH     STANDARD;      PRT;     4 AA.
AC   P19916;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-DEC-1992 (Rel. 24, Last annotation update)
DE   Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (Fragment).
OS   Pseudomonas carboxydohydrogena.
OC   Bacteria; Proteobacteria.
OX   NCBI_TaxID=290;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90055678; PubMed=2818128;
RA   Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT   "Homology and distribution of CO dehydrogenase structural genes in
RT   carboxydotrophic bacteria.";
RL   Arch. Microbiol. 152:335-341(1989).
CC   -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC       acceptor.
CC   -!- COFACTOR: MOLYBDENUM.
CC   -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC       SMALL.
DR   PIR; PL0140; PL0140.
KW   Oxidoreductase; Molybdenum.
FT   NON_TER       4       4
SQ   SEQUENCE   4 AA;  441 MW;  7761E876F0000000 CRC64;


  Query Match             8.7%;  Score 2;  DB 1;  Length 4;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          :
Db      1 M 1
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RESULT  29
DCMS_PSECH
ID   DCMS_PSECH     STANDARD;      PRT;     4 AA.
AC   P19918;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-DEC-1992 (Rel. 24, Last annotation update)
DE   Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (Fragment).
OS   Pseudomonas carboxydohydrogena.
OC   Bacteria; Proteobacteria.
OX   NCBI_TaxID=290;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90055678; PubMed=2818128;
RA   Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT   "Homology and distribution of CO dehydrogenase structural genes in
RT   carboxydotrophic bacteria.";
RL   Arch. Microbiol. 152:335-341(1989).
CC   -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC       acceptor.
CC   -!- COFACTOR: MOLYBDENUM.
CC   -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC       SMALL.
DR   PIR; PL0146; PL0146.
KW   Oxidoreductase; Molybdenum.
FT   NON_TER       4      4
SQ   SEQUENCE   4 AA;  420 MW;  6DD33DD6F0000000 CRC64;


  Query Match             8.7%;  Score 2;  DB 1;  Length 4;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          :
Db      1 M 1


RESULT  30
FAR4_HIRME
ID   FAR4_HIRME     STANDARD;      PRT;     4 AA.
AC   P42563;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFamide-like neuropeptide YMRF-amide.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX   NCBI_TaxID=6421;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  616 MW;  69D4068B30000000 CRC64;


  Query Match             8.7%;  Score 2;  DB 1;  Length 4;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          :
Db      2 M 2


RESULT  31
FMRF_MACNI
ID   FMRF_MACNI     STANDARD;      PRT;     4 AA.
AC   P01162;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS   Macrocallista nimbosa (Sun-ray clam),
OS   Nereis virens (Sandworm),
OS   Hirudo medicinalis (Medicinal leech), and
OS   Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC   Veneroidea; Veneridae; Macrocallista.
OX   NCBI_TaxID=6594, 6353, 6421, 27815;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
RX   MEDLINE=77215956; PubMed=877582;
RA   Price D.A., Greenberg M.J.;
RT   "Structure of a molluscan cardioexcitatory neuropeptide.";
RL   Science 197:670-671(1977).
RN   [2]
RP   SEQUENCE, AND CHARACTERIZATION.
RC   SPECIES=M.nimbosa; TISSUE=Ganglion;
RX   MEDLINE=78012038; PubMed=909875;
RA   Price D.A., Greenberg M.J.;
RT   "Purification and characterization of a cardioexcitatory neuropeptide
RT   from the central ganglia of a bivalve mollusc.";
RL   Prep. Biochem. 7:261-281(1977).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=N.virens;
RX   MEDLINE=90259866; PubMed=2342992;
RA   Krajniak K.G., Price D.A.;
RT   "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL   Peptides 11:75-77(1990).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=H.medicinalis;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [5]
RP   SEQUENCE.
RC   SPECIES=H.trivolvis; TISSUE=Kidney;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
CC       ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CC       CARDIAC CONTRACTION.
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
DR   PIR; A01426; ECNK.
DR   PIR; A60418; A60418.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  600 MW;  69D40699A0000000 CRC64;


  Query Match             8.7%;  Score 2;  DB 1;  Length 4;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          :
Db      2 M 2
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RESULT  32
BIOB_CITFR
ID   BIOB_CITFR     STANDARD;      PRT;     5 AA.
AC   P12997;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
GN   BIOB.
OS   Citrobacter freundii.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Citrobacter.
OX   NCBI_TaxID=546;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89006280; PubMed=2971595;
RA   Shiuan D., Campbell A.;
RT   "Transcriptional regulation and gene arrangement of Escherichia coli,
RT   Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL   Gene 67:203-211(1988).
CC   -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
CC   -!- PATHWAY: Biotin biosynthesis; last step.
CC   -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC       FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21922; -; NOT_ANNOTATED_CDS.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  532 MW;  75A5B1EDD6F00000 CRC64;


  Query Match             8.7%;  Score 2;  DB 1;  Length 5;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          :
Db      1 M 1


RESULT  33
BPP7_BOTIN
ID   BPP7_BOTIN     STANDARD;      PRT;     5 AA.
AC   P30425;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE   enzyme inhibitor).
OS   Bothrops insularis (Island jararaca) (Queimada jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8723;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=90351557; PubMed=2386615;
RA   Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT   "Primary structure and biological activity of bradykinin potentiating
RT   peptides from Bothrops insularis snake venom.";
RL   J. Protein Chem. 9:221-227(1990).
CC   -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC       ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC       BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC       IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR   PIR; G37196; G37196.
KW   Hypotensive agent; Venom.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   5 AA;  629 MW;  776DC37326B00000 CRC64;


  Query Match             8.7%;  Score 2;  DB 1;  Length 5;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          :
Db      1 Q 1


RESULT  34
GRWM_HUMAN
ID   GRWM_HUMAN     STANDARD;      PRT;     3 AA.
AC   P01157;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   Growth-modulating peptide.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77162369; PubMed=858356;
RA   Schlesinger D.H., Pickart L., Thaler M.M.;
RT   "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL   Experientia 33:324-325(1977).
CC   -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC       GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR   PIR; A01421; GKHU.
SQ   SEQUENCE   3 AA;  340 MW;  6331E81000000000 CRC64;


  Query Match             4.3%;  Score 1;  DB 1;  Length 3;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          :
Db      3 K 3


RESULT  35
FFKA_ANTEL
ID   FFKA_ANTEL     STANDARD;      PRT;     4 AA.
AC   P58705;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Antho-KAamide.
OS   Anthopleura elegantissima (Sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE.
RX   PubMed=1681803;
RA   Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT   "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
RT   novel neuropeptide from sea anemones.";
RL   Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN   [2]
RP   FUNCTION.
RX   PubMed=8397415;
RA   McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
```

```
RT   "The expansion behaviour of sea anemones may be coordinated by two
RT   inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC   -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC       groups. May be involved in the expansion phase of feeding
CC       behaviour in sea anemones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron-specific.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       L-3-PHENYLLACTYL.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  512 MW;  6DD339C9A0000000 CRC64;


  Query Match             4.3%;  Score 1;  DB 1;  Length 4;
  Best Local Similarity   0.0%;  Pred. No. 1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          :
Db      3 K 3


Search completed: June 10, 2002, 06:41:57
Job time: 240 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:37:17 ; Search time 25.17 Seconds
(without alignments)
34.365 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	30.4	4	11	Q08433	Q08433 rattus norv
2	7	30.4	5	13	P82070	P82070 litoria rub
3	6	26.1	5	2	P83073	P83073 bacillus ce
4	5	21.7	5	13	P82071	P82071 litoria rub
5	5	21.7	5	13	P82072	P82072 litoria rub
6	5	21.7	5	13	P82100	P82100 litoria rub
7	4	17.4	5	13	P82073	P82073 litoria rub
8	4	17.4	5	13	P82099	P82099 litoria rub
9	2	8.7	5	10	Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
Q08433
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCORONOSIDE.
CC -!- SUBCELLULAR LOCATION: MICROSOME.
DR EMBL; S38636; AAB19259.1; -.
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 30.4%; Score 7; DB 11; Length 4;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 il 3
:|
Db 2 VL 3

RESULT 2
P82070
ID P82070 PRELIMINARY; PRT; 5 AA.
AC P82070;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 30.4%; Score 7; DB 13; Length 5;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;

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  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 ld 4
          :|
Db      1 VD 2


RESULT   3
P83073
ID   P83073      PRELIMINARY;      PRT;     5 AA.
AC   P83073;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   88 KDA PROTEIN (FRAGMENT).
OS   Bacillus cereus.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1396;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=NCIMB 11796;
RA   Browne N., Dowds B.C.A.;
RL   Submitted (JUL-2001) to the SWISS-PROT data bank.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  623 MW;  6B01AAA336F00000 CRC64;


  Query Match             26.1%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 d 4
          |
Db      3 D 3


RESULT   4
P82071
ID   P82071      PRELIMINARY;      PRT;     5 AA.
AC   P82071;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  626 MW;  6DD9C9CB10300000 CRC64;


  Query Match             21.7%;  Score 5;  DB 13;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          |
Db      2 E 2


RESULT   5
P82072
ID   P82072      PRELIMINARY;      PRT;     5 AA.
AC   P82072;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 3.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  656 MW;  71A9C9CB10300000 CRC64;


  Query Match             21.7%;  Score 5;  DB 13;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 e 1
          |
Db      2 E 2


RESULT   6
P82100
ID   P82100      PRELIMINARY;      PRT;     5 AA.
AC   P82100;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ELECTRIN 4.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  616 MW;  61F2D1A059A00000 CRC64;


  Query Match             21.7%;  Score 5;  DB 13;  Length 5;
  Best Local Similarity   33.3%;  Pred. No. 5.6e+05;
  Matches    1;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy      3 ldv 5
          : |
Db      2 ITV 4


RESULT   7
P82073
ID   P82073      PRELIMINARY;      PRT;     5 AA.
AC   P82073;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 3.2.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  570 MW;  71A9C9C862A00000 CRC64;


  Query Match             17.4%;  Score 4;  DB 13;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 v 5
          |
Db      1 V 1


RESULT   8
P82099
ID   P82099      PRELIMINARY;      PRT;     5 AA.
AC   P82099;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ELECTRIN 3.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  630 MW;  668761F2C9A00000 CRC64;


  Query Match             17.4%;  Score 4;  DB 13;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 v 5
          |
Db      2 V 2


RESULT   9
Q99007
ID   Q99007      PRELIMINARY;      PRT;     5 AA.
AC   Q99007;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
GN   AMY1.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX   MEDLINE=91329704; PubMed=1831055;
RA   Jacobsen J.V., Close T.J.;
RT   "Control of transient expression of chimaeric genes by gibberellic
RT   acid and abscisic acid in protoplasts prepared from mature barley
RT   aleurone layers.";
RL   Plant Mol. Biol. 16:713-721(1991).
CC   -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC       LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
CC   -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC   -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC       BARLEY.
DR   EMBL; X54643; CAA38455.1; -.
KW   Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW   Calcium; Multigene family.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  600 MW;  61E3344DD6F00000 CRC64;


  Query Match              8.7%;  Score 2;  DB 10;  Length 5;
  Best Local Similarity    0.0%;  Pred. No. 5.6e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 l 3
          :
Db      1 M 1



Search completed: June 10, 2002, 06:41:24
Job time: 247 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:36:38 ; Search time 24.27 Seconds
(without alignments)
22.883 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 21101

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_032802:*
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11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	100.0	5	17	AAR95719	Alpha-4Beta-1 inte
2	23	100.0	5	18	AAW25192	LDV-peptide capabl
3	23	100.0	5	19	AAW46318	Peptide recognised
4	23	100.0	5	20	AAY03855	Integrin ligand di
5	23	100.0	5	21	AAY80488	Cell adhesion pept
6	23	100.0	5	21	AAY77442	Fibronectin CS1-de
7	23	100.0	5	21	AAY69619	VLA-4 inhibitor pe
8	23	100.0	5	22	AAB73465	Fibronectin VLA-4
9	23	100.0	5	22	AAB91966	Fibronectin fragme
10	23	100.0	5	22	AAB50876	Integrin recogniti
11	23	100.0	5	22	AAB59135	Peptide #3 recogni
12	19	82.6	5	17	AAR99752	Cyclic peptide inh
13	18	78.3	4	21	AAY77441	Fibronectin CS1-de
14	18	78.3	4	21	AAY51252	Cyclizing peptide
15	18	78.3	5	16	AAW01724	Inhibitor of fibro
16	18	78.3	5	18	AAW45730	Precursor peptide
17	18	78.3	5	21	AAY77428	Fibronectin CS1 pe
18	18	78.3	5	21	AAY77431	Fibronectin CS1 pe
19	17	73.9	5	17	AAR92849	Cell adhesion modu
20	16	69.6	5	17	AAR95707	Alpha-4Beta-1 inte
21	16	69.6	5	17	AAR95716	Alpha-4Beta-1 inte
22	16	69.6	5	17	AAR95717	Alpha-4Beta-1 inte
23	16	69.6	5	17	AAR99748	Cyclic peptide inh
24	16	69.6	5	18	AAW45731	Precursor peptide
25	16	69.6	5	20	AAY30308	Angiopoietin deriv
26	14	60.9	3	16	AAR82907	Non-RGD, non-YISGR
27	14	60.9	3	18	AAW25187	LDV-peptide capabl
28	14	60.9	3	21	AAB01568	Cell binding domai
29	14	60.9	3	22	AAB91984	Fibronectin fragme
30	14	60.9	4	10	AAP91609	Motif useful in to
31	14	60.9	4	16	AAW01711	Inhibitor of fibro
32	14	60.9	4	16	AAR66483	Sodium channel gen
33	14	60.9	4	17	AAR95728	Alpha-4Beta-1 inte
34	14	60.9	4	17	AAR95731	Alpha-4Beta-1 inte
35	14	60.9	4	17	AAR95726	Alpha-4Beta-1 inte
36	14	60.9	4	17	AAR95704	Alpha-4Beta-1 inte
37	14	60.9	4	17	AAR95714	Alpha-4Beta-1 inte
38	14	60.9	4	19	AAW55750	Immunisation motif
39	14	60.9	4	21	AAG80707	Fibronectin-derive
40	14	60.9	4	21	AAY77420	Fibronectin CS1 pe
41	14	60.9	4	22	AAB81415	Integrin alpha4bet
42	14	60.9	4	22	AAB59922	Human leptin fragm
43	14	60.9	5	6	AAP50562	Sequence of peptid
44	14	60.9	5	14	AAR33614	Pseudopeptide rhym
45	14	60.9	5	14	AAR31940	In vivo tumour bin
46	14	60.9	5	15	AAR59983	Peptide signal seq
47	14	60.9	5	16	AAW01722	Inhibitor of fibro
48	14	60.9	5	16	AAW01718	Inhibitor of fibro
49	14	60.9	5	17	AAR95708	Alpha-4Beta-1 inte
50	14	60.9	5	17	AAR91725	NAP subsequence.
51	14	60.9	5	17	AAR99756	Cyclic peptide inh
52	14	60.9	5	17	AAR99757	Cyclic peptide inh
53	14	60.9	5	17	AAW00406	Interleukin-6 anta
54	14	60.9	5	18	AAY02055	Peptide used to pr
55	14	60.9	5	18	AAW25189	LDV-peptide capabl
56	14	60.9	5	18	AAW25191	LDV-peptide capabl
57	14	60.9	5	19	AAW46813	Endo-beta1,4-gluca
58	14	60.9	5	20	AAY30444	Nematode extracted
59	14	60.9	5	20	AAW88079	Inhibitor peptide
60	14	60.9	5	21	AAB15329	NAP domain fragmen
61	14	60.9	5	21	AAB08242	Peptide derived fr
62	14	60.9	5	21	AAY93436	Peptide motif from
63	14	60.9	5	21	AAY82724	Peptide cyclo-(Leu
64	14	60.9	5	21	AAY87605	N. denitrificans a
65	14	60.9	5	21	AAY80491	Cell adhesion pept
66	14	60.9	5	21	AAY77427	Fibronectin CS1 pe
67	14	60.9	5	21	AAY69620	VLA-4 inhibitor pe
68	14	60.9	5	22	AAB73466	Fibronectin VLA-4
69	14	60.9	5	22	AAB91985	Fibronectin fragme
70	13	56.5	4	21	AAY94573	Peptide based endo
71	13	56.5	4	21	AAY43756	Amino acid sequenc
72	13	56.5	4	22	AAB30758	Peptide which is u
73	13	56.5	5	13	AAR31316	Alpha-substituted
74	13	56.5	5	13	AAR29448	Endothelin antagon
75	13	56.5	5	13	AAR29449	Endothelin antagon
76	13	56.5	5	13	AAR29450	Endothelin antagon
77	13	56.5	5	13	AAR29451	Endothelin antagon
78	13	56.5	5	13	AAR29452	Endothelin antagon
79	13	56.5	5	15	AAR54601	Cholecystokinin an
80	13	56.5	5	15	AAR54602	Cholecystokinin an
81	13	56.5	5	15	AAR54603	Cholecystokinin an
82	13	56.5	5	15	AAR54604	Cholecystokinin an
83	13	56.5	5	15	AAR54605	Cholecystokinin an
84	13	56.5	5	15	AAR69220	Endothelin C-termi

85	13	56.5	5	15	AAR69221	Endothelin C-termi
86	13	56.5	5	15	AAR69222	Endothelin C-termi
87	13	56.5	5	15	AAR69223	Endothelin C-termi
88	13	56.5	5	15	AAR69224	Endothelin C-termi
89	13	56.5	5	15	AAR69236	Endothelin C-termi
90	13	56.5	5	16	AAW01727	Inhibitor of fibro
91	13	56.5	5	19	AAW69701	HCAR and MCAR pept
92	13	56.5	5	19	AAW65871	Endothelin recepto
93	13	56.5	5	19	AAW53604	Osteopontin derive
94	13	56.5	5	21	AAB28654	Chemotactic peptid
95	13	56.5	5	21	AAB28658	Chemotactic peptid
96	13	56.5	5	21	AAB28669	Chemotactic peptid
97	13	56.5	5	21	AAB28670	Chemotactic peptid
98	13	56.5	5	21	AAY83335	D region motif of
99	13	56.5	5	21	AAY77432	Fibronectin CS1 pe
100	13	56.5	5	21	AAY69538	Bioactive peptide

ALIGNMENTS

RESULT 1
AAR95719
ID AAR95719 standard; peptide; 5 AA.
XX
AC AAR95719;
XX
DT 04-DEC-1996 (first entry)
XX
DE Alpha-4Beta-1 integrin binding inhibitory peptide 16.
XX
KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW inhibitor; binding; white blood cell; migration; capillary wall;
KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW CS1; CS5; H1; LDV; active site.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 5
FT /note= "Val-NH2"
XX
PN US5510332-A.
XX
PD 23-APR-1996.
XX
PF 07-JUL-1994; 94US-0271830.
XX
PR 07-JUL-1994; 94US-0271830.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Beck PJ, Kogan TP, Ren K, Vanderslice P;
XX
DR WPI; 1996-221274/22.
XX
PT New peptide(s) based on the LDV domain of fibronectin - used for
PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT fibronectin or invasin
XX
PS Disclosure; Column 21-22; 35pp; English.
XX
CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
CC surface of endothelial cells that line the interior wall of capillaries.
CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
CC white blood cells to adhere to the capillary wall in areas where the
CC tissue surrounding the capillary has been infected or damaged. Sometimes
CC this white blood cell migration can become uncontrolled, with white
CC blood cells flooding to the scene, causing widespread tissue damage.
CC Cpds. capable of blocking this process may be beneficial as therapeutic
CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC fibronectin. Three distinct IA4B1-binding sites have been identified
CC within fibronectin. One site is found in the HeplI region and is
CC expressed in all isoforms; two others (CS1 and CS5) are present in the
CC alternatively spliced type III connecting segments. CS1 has the higher
CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC peptide that include the LDV domain presented in such a way by its novel
CC flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 2
AAW25192
ID AAW25192 standard; peptide; 5 AA.
XX
AC AAW25192;
XX
DT 05-JAN-1998 (first entry)
XX
DE LDV-peptide capable of binding cell adhesion molecules.
XX
KW LDV; leucine; aspartic acid; valine; cell adhesion molecule;
KW binding; bladder irrigation; tumour removal; endoscopic operation;
KW transurethral resection; cancer; neoplasia.
XX
OS Synthetic.
XX
PN DE19529909-A1.
XX
PD 20-FEB-1997.
XX
PF 15-AUG-1995; 95DE-1029909.
XX
PR 15-AUG-1995; 95DE-1029909.
XX
PA (FREP) FRESENIUS AG.
XX
PI Boehle A;
XX
DR WPI; 1997-133793/13.
XX
PT Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
PT adhesion molecules
XX
PS Claim 6; Page 8; 8pp; German.
XX
CC AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
CC The peptides are capable of binding to cell adhesion molecules and
CC are used in aqueous irrigation solutions for use during and after
CC endoscopic operations. Preferred irrigation solutions are
CC electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
CC oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
CC GPRP, VTL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid
CC code). The solutions are especially used for irrigating the bladder
CC during and after tumour removal by transurethral resection. The
CC peptides protect against recurrence of tumours.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   3
AAW46318
ID   AAW46318 standard; Protein; 5 AA.
XX
AC   AAW46318;
XX
DT   08-MAY-1998  (first entry)
XX
DE   Peptide recognised by integrin alpha4etal.
XX
KW   Fibrinogen; integrin; alpha-IIb-beta3; cell surface receptor;
KW   penton base protein; coat proteins; adenovirus; binding site;
KW   cellular adhesion; extracellular matrix molecule; binding domain;
KW   cell surface binding site; bispecific molecule; gene therapy.
XX
OS   Unidentified.
XX
PN   US5712136-A.
XX
PD   27-JAN-1998.
XX
PF   17-APR-1996;   96US-0634060.
XX
PR   08-SEP-1994;   94US-0303162.
XX
PA   (GENV-) GENVEC INC.
XX
PI   Brough DE,  Bruder JT,  Kovesdi I,  McVey DL,  Roelvink PW;
PI   Wickham TJ;
XX
DR   WPI; 1998-119984/11.
XX
PT   Methods for introducing adenovirus into cells - used for genetic
PT   engineering and gene therapy
XX
PS   Claim 27; Column 2; 56pp; English.
XX
CC   The present sequence is a linear stretch of amino acids (present in
CC   fibronectin) recognised by the integrin alpha4beta1. Integrins are
CC   cell surface receptors. The penton base protein (one of the coat
CC   proteins) of adenoviruses binds to integrins. The integrins not only
CC   provide a binding site for the adenoviral penton base protein, but also
CC   mediate cellular adhesion to the extracellular matrix molecules. The
CC   specification describes a method of introducing an adenovirus into
CC   a cell in vitro having a particular cell surface binding site. The
CC   adenovirus is contacted with a bispecific molecule comprising a component
CC   that selectively binds a binding domain of the penton base protein of the
CC   adenovirus and a second component that selectively binds the cell surface
CC   binding site. A complex of the adenovirus and the bispecific molecule is
CC   formed, and the  cell is contacted with it to allow entry of the
CC   adenovirus into the cell. The methods can be used for research and the
CC   vectors can be used for gene therapy.
XX
SQ   Sequence   5 AA;


  Query Match           100.0%;  Score 23;  DB 19;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   4
AAY03855
ID   AAY03855 standard; peptide; 5 AA.
XX
AC   AAY03855;
XX
DT   16-JUN-1999  (first entry)
XX
DE   Integrin ligand dissociator (ILD) peptide.
XX
KW   Integrin-ligand; dissociator; disaggregation; platelet thrombus; stroke;
KW   fibrinogen; glycoprotein IIb-IIIa; angina; myocardial infarction; bone;
KW   osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy;
KW   psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
KW   organ transplant rejection; arthritis; ILD.
XX
OS   Synthetic.
XX
PN   WO9911280-A1.
XX
PD   11-MAR-1999.
XX
PF   03-SEP-1998;   98WO-US18305.
XX
PR   03-SEP-1997;   97US-0057463.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Hu DD,  Smith JW;
XX
DR   WPI; 1999-243586/20.
XX
PT   Disaggregating a ligand:integrin receptor complex
XX
PS   Disclosure; Page 10; 39pp; English.
XX
CC   The invention relates to integrin ligand dissociators. Disaggregation of
CC   an existing platelet thrombus in a blood vessel is due to dissociation of
CC   fibrinogen from glycoprotein IIb-IIIa. This dissociation is caused by the
CC   binding of an integrin-ligand dissociator at ligand binding site I of
CC   glycoprotein IIb-IIIa. The invention provides a method of disaggregating
CC   an existing platelet thrombus in a blood vessel, where the platelet
CC   thrombus may form an occlusion of a blood vessel, in a subject comprises
CC   administering a compound which dissociates fibrinogen bound to a first
CC   site on platelet glycoprotein IIb-IIIa, by binding to a second
CC   interacting site on platelet glycoprotein IIb-IIIa, disaggregating the
CC   platelet thrombus. The method is used to treat humans with unstable
CC   angina, stroke and/or acute myocardial infarction. The methods can be
CC   used to enact de-adhesion of osteoclasts from the bone surface to halt
CC   bone loss in a patient with osteoporosis. The methods can also be used
CC   for the de-adhesion of angiogenic endothelial cells in a patient with a
CC   pathologic condition associated with angiogenesis, e.g. cancer, diabetic
CC   retinopathy, psoriasis. The methods can also be used to treat tumours,
CC   atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory
CC   bowel disease, or organ transplant rejection, and asthma. The methods can
CC   be used for the dissolution of pre-formed platelet aggregates, which is a
CC   departure from the current strategy of treatment prior to formation of
CC   vascular occlusions.  The present sequence represents an integrin ligand
CC   dissociator (ILD) that can be used in the method of the invention.
XX
SQ   Sequence   5 AA;


  Query Match           100.0%;  Score 23;  DB 20;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT   5
AAY80488
ID   AAY80488 standard; peptide; 5 AA.
```

XX
AC AAY80488;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cell adhesion peptide #23.
XX
KW Bone regenerative; osteopathic; osseous tissue; reconstitution;
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.
XX
OS Synthetic.
XX
PN WO200004941-A1.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16800.
XX
PR 24-JUL-1998; 98US-0122348.
XX
PA (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
XX
PI Budny JA;
XX
DR WPI; 2000-195084/17.
XX
PT System for reconstructing osseous tissue, useful e.g. for treating
PT fractures, comprises scaffold containing promoter of bone formation and
PT inhibitor of bone resorption -
XX
PS Claim 14; Page 32; 44pp; English.
XX
CC The invention relates to a novel system for reconstitution of osseous
CC tissue comprising a scaffold carrying a compound (I) that promotes
CC bone formation and a component that decreases bone resorption (II).
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular
CC matrix. (I) is preferably selected from: selectin or selectin binding
CC fragments, proteins and peptides that facilitate cell adhesion,
CC plasminogen activator inhibitors, protease inhibitors and
CC metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed
CC examples of cell adhesion peptides used in the system of the invention.
CC The system is used to replace, remodel or correct bone defects, e.g.
CC fractures, fissures or bone mass loss. Incorporation of (I) into the
CC scaffold results in rapid seeding by osteoblasts and the development of
CC an organic matrix, i.e. the preformed scaffold replaces the
CC rate-determining step of extracellular matrix formation. The scaffold can
CC be designed to have a predetermined resorption/degradation rate, and may
CC include regulatory compounds for specific cell types.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 6
AAY77442
ID AAY77442 standard; peptide; 5 AA.
XX
AC AAY77442;
XX
DT 22-MAY-2000 (first entry)
XX
DE Fibronectin CS1-derived peptide #33.
XX

KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS Mammalia.
XX
PN WO200002903-A1.
XX
PD 20-JAN-2000.
XX
PF 15-DEC-1998; 98WO-US26605.
XX
PR 10-JUL-1998; 98US-0113689.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX
DR WPI; 2000-182213/16.
XX
PT New peptidomimetic compounds used as cell surface fibronectin
PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT cardiovascular disorders -
XX
PS Disclosure; Fig 2; 243pp; English.
XX
CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC important role in the maturation and trafficking. VLA-4-mediated
CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC critical step in the inflammatory response. The peptidomimetics of the
CC invention may be used to treat both chronic and acute immunoinflammatory
CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC allograft rejection. They may also be used to treat psoriasis and other
CC skin inflammations, demyelinating diseases of the central nervous system
CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC diabetes, inflammatory bowel disease, kidney inflammation and
CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC immune response on repeated administration, or the 25-mer CS-1 peptide,
CC which is large and costly to make and is subject to rapid proteolytic
CC degradation. The peptidomimetics of the invention are smaller in
CC comparison to the CS-1 peptide and therefore less expensive to
CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC (AAY77410).
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 7
AAY69619
ID AAY69619 standard; peptide; 5 AA.
XX
AC AAY69619;
XX
DT 19-APR-2000 (first entry)
XX
DE VLA-4 inhibitor peptide #2.
XX

KW LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1;
KW CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative;
KW arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder;
KW autoimmune disorder; respiratory disorder; LDV motif.
XX
OS Synthetic.
XX
PN WO200000477-A1.
XX
PD 06-JAN-2000.
XX
PF 31-MAY-1999; 99WO-IB00973.
XX
PR 30-JUN-1998; 98US-0091180.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Duplantier AJ, Milici AJ, Chupak LS;
XX
DR WPI; 2000-126762/11.
XX
PT Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives -
XX
PS Disclosure; Page 2; 120pp; English.
XX
CC The invention relates to novel arylalkyl and arylureidoalkyl
CC azolylalkanoic acid derivatives and related compounds (I), and their
CC salts and prodrugs. These are are integrin inhibitors, specifically of
CC VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29),
CC which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
CC inducible cell surface protein VCAM-1 (vascular cell adhesion
CC molecule-1) and for the alternatively spliced forms of fibronectin (FN)
CC which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
CC and consequent or associated pathogenic processes mediated by VLA-4, and
CC may therefore be useful in the treatment and prevention of inflammatory,
CC autoimmune, or respiratory disorders . These include asthma, arthritis,
CC psoriasis, multiple sclerosis, transplant rejection, diabetes, and
CC inflammatory bowel disease. Sequences AAY69618-Y69620 represent peptides
CC derived from the VLA-4-binding domain of the FN CS-1 region which
CC contain the LDV motif and are known to inhibit fibronectin-dependent
CC cell adhesion.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 8
AAB73465
ID AAB73465 standard; peptide; 5 AA.
XX
AC AAB73465;
XX
DT 02-JUL-2001 (first entry)
XX
DE Fibronectin VLA-4 binding domain-derived pentapeptide #1.
XX
KW Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
KW very late antigen; antibody; kidney disease; chronic renal failure;
KW end-stage renal disease; chronic diabetic nephropathy;
KW diabetic glomerulopathy; diabetic renal hypertrophy;
KW hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
KW chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
KW nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
XX
OS Unidentified.

XX
PN WO200119396-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US25140.
XX
PR 14-SEP-1999; 99US-0153826.
XX
PA (BIOJ) BIOGEN INC.
PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
XX
PI Allen A, Pusey C, Lobb R;
XX
DR WPI; 2001-273408/28.
XX
PT Treating a mammal in, or at a risk of developing, chronic renal
PT failure, involves administering at least one integrin antagonist to the
PT mammal -
XX
PS Disclosure; Page 24; 62pp; English.
XX
CC The invention relates to a method for treating a mammal with,
CC or at risk of developing, chronic renal failure, involving the
CC administration of at least one integrin antagonist. The integrin
CC antagonists that may be used in the method include antagonists of
CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
CC containing integrins. In particular, the antagonists are antibodies
CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in
CC the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).
CC The method of the invention may be used to treat chronic renal failure,
CC end-stage renal disease, chronic diabetic nephropathy, diabetic
CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
CC hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary
CC nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
CC peptides derived from the VLA-4 binding domain (CS-1 region) of
CC fibronectin, which inhibit fibronectin-dependent cell adhesion, and may
CC therefore be used in the method of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 9
AAB91966
ID AAB91966 standard; Peptide; 5 AA.
XX
AC AAB91966;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1142.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.

XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 569; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 10
AAB50876
ID AAB50876 standard; peptide; 5 AA.
XX
AC AAB50876;
XX
DT 19-MAR-2001 (first entry)
XX
DE Integrin recognition peptide sequence #3.
XX
KW Integrin; transmembrane protein; alpha4 integrin inhibitor;
KW paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
KW multiple sclerosis; asthma; atherosclerosis; wound healing.
XX
OS Unidentified.
XX
PN WO200073342-A1.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15153.
XX
PR 01-JUN-1999; 99US-0323447.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ginsberg MH, Pfaff M, Liu S;
XX
DR WPI; 2001-070959/08.
XX
PT Polypeptides useful in construction of structural models for
PT identifying therapeutic compounds, comprises series of heptad repeats
PT that mimic a transmembrane domain and cytoplasmic domain attached to
PT heptad repeats -
XX
PS Disclosure; Page 2; 37pp; English.
XX
CC The present sequence is given in a specification relating to a
CC polypeptide comprising a series of heptad-repeats that mimic a
CC transmembrane domain, and a selected cytoplasmic domain attached to the
CC heptad repeats. At least a portion of the polypeptide is prepared
CC recombinantly or at least 1 heptad repeat in the series has a different
CC amino acid sequence to other heptad repeats in the series. The
CC polypeptide is useful in the construction of structural models which are
CC useful for evaluating structure and activity of a selected occupied and
CC clustered transmembrane protein having the selected cytoplasmic domain
CC and for identifying therapeutic compounds. It is also useful for
CC identifying agents as inhibitors of alpha4 integrin biological
CC responses by contacting the structural model with paxillin or a
CC paxillin related molecule in the presence and absence of a test agent
CC and determining binding of paxillin or paxillin related molecule to the
CC structural model. A decrease in binding in the presence of the test
CC agent indicates that the test agent is an inhibitor of alpha4 integrin
CC biological response. Inhibitors of the binding of paxillin to alpha4 are
CC useful in blocking immune responses in conditions such as inflammatory
CC bowel disease, arthritis, multiple sclerosis and asthma and in
CC inhibiting atherosclerosis and scarring during wound healing.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 eildv 5
|||||
Db 1 eildv 5

RESULT 11
AAB59135
ID AAB59135 standard; peptide; 5 AA.
XX
AC AAB59135;
XX
DT 21-MAR-2001 (first entry)
XX
DE Peptide #3 recognised by integrin.
XX
KW Heptad repeat; transmembrane domain; cytoplasmic; integrin;
KW inflammation; thrombosis; malignancy.
XX
OS Synthetic.
XX
PN WO200073341-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14656.
XX
PR 27-MAY-1999; 99US-0320907.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ginsberg MH, Pfaff M;
XX

```
DR   WPI; 2001-041143/05.
XX
PT   Polypeptides useful in construction of structural models for
PT   identifying therapeutic compounds, comprises series of heptad repeats
PT   that mimic a transmembrane domain and cytoplasmic domain attached to
PT   the repeats -
XX
PS   Disclosure; Page 2; 36pp; English.
XX
CC   The present invention relates to a peptide with a series of
CC   heptad-repeats that mimic a transmembrane domain and a selected
CC   cytoplasmic domain attached to the heptad repeats. The invention
CC   is useful for evaluating structure and activity of a selected
CC   occupied and clustered transmembrane protein with the selected
CC   cytoplasmic domain and for identifying therapeutic compounds. It
CC   is also useful for identifying a cytoplasmic domain binding partner.
CC   It is may be used to study protein interactions with transmembrane
CC   proteins such as integrin, which can be used to treat conditions in
CC   which over activity of integrins is involved, such as inflammation,
CC   thrombosis and malignancy.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 23;  DB 22;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 eildv 5


RESULT  12
AAR99752
ID   AAR99752 standard; peptide; 5 AA.
XX
AC   AAR99752;
XX
DT   02-SEP-1996  (first entry)
XX
DE   Cyclic peptide inhibitor of alpha-4/beta-1 integrin binding to VCAM-1.
XX
KW   Vascular cell adhesion molecule 1; integrin; fibronectin; invasin;
KW   binding inhibitor; atherosclerosis; allergy; rheumatoid arthritis;
KW   asthma; multiple sclerosis; type 1 diabetes; cancer; cyclic;
KW   white blood cell; metastasis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "cross-link between Glu at position 1 and
FT                          Val at position 5"
FT   Modified-site   5
FT                   /note= "cross-link between Glu at position 1 and
FT                          Val at position 5"
XX
PN   WO9600581-A1.
XX
PD   11-JAN-1996.
XX
PF   27-JUN-1995;   95WO-US08353.
XX
PR   29-JUN-1994;   94US-0268192.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Beck PJ,  Kogan TP,  Ren K,  Vanderslice P;
XX
DR   WPI; 1996-077338/08.
XX
PT   Isolated, purified cyclic peptide which inhibits binding of alpha-4
PT   beta-1 integrin to VCAM-1 or fibronectin - useful for treating e.g.
PT   atherosclerosis or allergy
XX
PS   Claim 6; Page 28; 51pp; English.
XX
CC   AAR99746-R99785 are cyclic peptides which selectively inhibit binding
CC   of alpha4beta1 integrin to proteins such as vascular cell adhesion
CC   molecule 1 (VCAM-1), fibronectin and invasin. Due to this action the
CC   peptides are useful in pharmaceutical prepns. for the treatment of
CC   such ailments as asthma, atherosclerosis, rheumatoid arthritis,
CC   allergy, multiple sclerosis, type 1 diabetes and certain cancers
CC   (e.g. leukaemia, melanoma, lymphoma and sarcoma), as cell adhesion
CC   involving the alpha4beta1 integrin is believed to be involved in
CC   metastasis.
XX
SQ   Sequence   5 AA;


  Query Match             82.6%;  Score 19;  DB 17;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          | |||
Db      1 efldv 5


RESULT  13
AAY77441
ID   AAY77441 standard; peptide; 4 AA.
XX
AC   AAY77441;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Fibronectin CS1-derived peptide #32.
XX
KW   Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW   CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW   inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS   Mammalia.
XX
PN   WO200002903-A1.
XX
PD   20-JAN-2000.
XX
PF   15-DEC-1998;   98WO-US26605.
XX
PR   10-JUL-1998;   98US-0113689.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Arrhenius TS,  Elices MJ,  Gaeta FCA,  He Y,  Huyghe BG,  Chen PG;
XX
DR   WPI; 2000-182213/16.
XX
PT   New peptidomimetic compounds used as cell surface fibronectin
PT   expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT   cardiovascular disorders -
XX
PS   Disclosure; Fig 2; 243pp; English.
XX
CC   The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC   capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC   CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC   the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC   the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC   important role in the maturation and trafficking. VLA-4-mediated
CC   leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC   critical step in the inflammatory response. The peptidomimetics of the
CC   invention may be used to treat both chronic and acute immunoinflammatory
CC   conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
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CC   allograft rejection. They may also be used to treat psoriasis and other
CC   skin inflammations, demyelinating diseases of the central nervous system
CC   (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC   diabetes, inflammatory bowel disease, kidney inflammation and
CC   restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC   involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC   immune response on repeated administration, or the 25-mer CS-1 peptide,
CC   which is large and costly to make and is subject to rapid proteolytic
CC   degradation. The peptidomimetics of the invention are smaller in
CC   comparison to the CS-1 peptide and therefore less expensive to
CC   manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
CC   and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
CC   their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
CC   (AAY77410).
XX
SQ   Sequence   4 AA;


  Query Match             78.3%;  Score 18;  DB 21;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ildv 4


RESULT  14
AAY51252
ID   AAY51252 standard; peptide; 4 AA.
XX
AC   AAY51252;
XX
DT   14-APR-2000  (first entry)
XX
DE   Cyclizing peptide 1.
XX
KW   Cyclization; propanesulfonic acid anhydride; somatostatin agonist;
KW   L-363,301.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   3
FT                   /note= "Asp(O-tBu)"
FT   Modified-site   4
FT                   /note= "Val-NH(CH2)5COOH"
XX
PN   DE19824449-A1.
XX
PD   02-DEC-1999.
XX
PF   30-MAY-1998;   98DE-1024449.
XX
PR   30-MAY-1998;   98DE-1024449.
XX
PA   (CLRN ) CLARIANT GMBH.
XX
PI   Mollenkopf CC,  Henklein P;
XX
DR   WPI; 2000-107180/10.
XX
PT   Cyclization of penta- or hexapeptides, e.g. to prepare somatostatin
PT   agonist -
XX
PS   Claim 2; Page 4; 6pp; German.
XX
CC   This invention describes a novel method for the cyclization of penta- or
CC   hexapeptides which is effected by reaction with propanesulfonic acid
CC   anhydride (I). The process is especially useful for cyclizing
CC   H-Phe-D-Trp-Ala-Thr(tBu)-Phe-Pro-OH to obtain the somatostatin agonist
CC   L-363,301, or for cyclizing H-Ile-Leu-Asp(OtBu)-Val-NH(CH_2)_5COOH. The
CC   process gives higher yields than prior art processes. This sequence
CC   represents a peptide used to illustrate the method of the invention.
XX
SQ   Sequence   4 AA;


  Query Match             78.3%;  Score 18;  DB 21;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ildv 4


RESULT  15
AAW01724
ID   AAW01724 standard; peptide; 5 AA.
XX
AC   AAW01724;
XX
DT   16-APR-1997  (first entry)
XX
DE   Inhibitor of fibronectin CS-1 peptide and VLA-4 receptor binding.
XX
KW   fibronectin; high affinity; CS-1; recognition sequence; VLA-4;
KW   alpha-4 beta-1 cell adhesion receptor; CD49d/CD29; inhibitor;
KW   leukocyte trafficking function; peptidomimetic; treatment; asthma;
KW   rheumatoid arthritis; osteoarthritis; allograft rejection;
KW   skin inflammation; central nervous system demyelinating disease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "optionally D-Ile"
FT   Modified-site   5
FT                   /note= "Pro, D-Pro-NH2 or Pro-NH2"
XX
PN   WO9515973-A1.
XX
PD   15-JUN-1995.
XX
PF   05-DEC-1994;   94WO-US13943.
XX
PR   02-DEC-1994;   94US-0164101.
PR   06-DEC-1993;   93US-0164101.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Arrhenius TS,  Elices MJ,  Gaeta FCA;
XX
DR   WPI; 1995-224284/29.
XX
PT   New peptide mimics of fibronectin CS-1 sequence - inhibit
PT   interaction of endothelial cells and VLA-4 carrying inflammatory
PT   cells, for treating or preventing asthma, arthritis etc.
XX
PS   Disclosure; Page 37; 103pp; English.
XX
CC   The alpha-4 beta-1 (CD49d/CD29, VLA-4) cell adhesion receptor is an
CC   active participant in leukocyte trafficking functions. Binding of
CC   inflammatory cells to endothelial cells that express the CS-1 portion
CC   (AAW01703) of fibronectin on their surfaces can be inhibited by CS-1
CC   peptidomimetic cpds. of minimal length. A minimal essential sequence for
CC   specific VLA-4 recognition of CS-1 has been identified as the tripeptide
CC   LDV. A generic peptidomimetic inhibits the binding of Jurkat cells
CC   (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay
CC   in an aq. buffer at a pH value of 7.2-7.4 to an extent that is equal to
CC   or upto about 3000-fold greater than the inhibition in the binding
CC   exhibited by AAW01705. CS-1 mediated inflammation, e.g. asthma,
CC   rheumatoid arthritis, osteoarthritis, allograft rejection, skin
CC   inflammation or central nervous system demyelinating disease, can be
CC   treated by the peptidomimetics. AAW01706-27 are exemplary inhibitor
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CC   peptides.
XX
SQ   Sequence   5 AA;


  Query Match             78.3%;  Score 18;  DB 16;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ildv 4


RESULT  16
AAW45730
ID   AAW45730 standard; peptide; 5 AA.
XX
AC   AAW45730;
XX
DT   17-JUN-1998  (first entry)
XX
DE   Precursor peptide #1.
XX
KW   Cyclic peptide; dimeric peptide; vascular cell adhesion molecule-1;
KW   VCAM-1; fibronectin; integrin; rheumatoid arthritis; asthma;
KW   multiple sclerosis; VLA-4; very late antigen-4; precursor.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   3
FT                   /note= "Asp(OBut)"
FT   Modified-site   5
FT                   /note= "Piperazinyl-1-yl-acetic acid"
XX
PN   WO9702289-A1.
XX
PD   23-JAN-1997.
XX
PF   02-JUL-1996;   96WO-GB01580.
XX
PR   01-JUN-1996;   96GB-0011470.
PR   06-JUL-1995;   95GB-0013798.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Dutta AS;
XX
DR   WPI; 1997-108916/10.
XX
PT   Cyclic octa:peptide comprising dimeric tetra:peptides joined by two
PT   peptide mimetic linking gps. - block interaction of VCAM-1 and/or
PT   fibronectin with integrin VLA4, used in treating arthritis, asthma
PT   and multiple sclerosis
XX
PS   Example 1; Page 30; 82pp; English.
XX
CC   The present sequence represents a precursor peptide. The invention
CC   relates to cyclic peptides which block the interaction of protein
CC   ligand VCAM-1 (vascular cell adhesion molecule-1) to its integrin
CC   receptor VLA-4 (very late antigen-4), thereby modulating T-cell
CC   proliferation, B-cell localisation to germinal centres and adhesion of
CC   activated T-cells and eosinophils to endothelial cells. These peptides
CC   are thus of use in treating diseases associated with these processes,
CC   including rheumatoid arthritis, multiple sclerosis and asthma, melanoma
CC   cell invasion in metastasis, autoimmune diabetes, colitis, autoimmune
CC   encephalomyelitis, atherosclerosis, peripheral vascular or
CC   cardiovascular disease, nephritis, allograft rejection, psoriasis,
CC   restenosis, myocarditis, and inflammatory bowel disease.
XX
SQ   Sequence   5 AA;


  Query Match             78.3%;  Score 18;  DB 18;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ildv 4


RESULT  17
AAY77428
ID   AAY77428 standard; peptide; 5 AA.
XX
AC   AAY77428;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Fibronectin CS1 peptidomimetic #19.
XX
KW   Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW   CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW   inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   5
FT                   /note= "C-terminal amide, D-form residue"
XX
PN   WO200002903-A1.
XX
PD   20-JAN-2000.
XX
PF   15-DEC-1998;   98WO-US26605.
XX
PR   10-JUL-1998;   98US-0113689.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Arrhenius TS,  Elices MJ,  Gaeta FCA,  He Y,  Huyghe BG,  Chen PG;
XX
DR   WPI; 2000-182213/16.
XX
PT   New peptidomimetic compounds used as cell surface fibronectin
PT   expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT   cardiovascular disorders -
XX
PS   Disclosure; Page 136; 243pp; English.
XX
CC   The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC   capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC   CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC   the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC   the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC   important role in the maturation and trafficking. VLA-4-mediated
CC   leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC   critical step in the inflammatory response. The peptidomimetics of the
CC   invention may be used to treat both chronic and acute immunoinflammatory
CC   conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC   allograft rejection. They may also be used to treat psoriasis and other
CC   skin inflammations, demyelinating diseases of the central nervous system
CC   (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC   diabetes, inflammatory bowel disease, kidney inflammation and
CC   restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC   involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC   immune response on repeated administration, or the 25-mer CS-1 peptide,
CC   which is large and costly to make and is subject to rapid proteolytic
CC   degradation. The peptidomimetics of the invention are smaller in
CC   comparison to the CS-1 peptide and therefore less expensive to
CC   manufacture, and are resistant to proteolysis. Sequences AAY77415-Y77433
CC   represent specific examples of the inhibitory peptidomimetics of the
CC   invention.
```

```
XX
SQ   Sequence   5 AA;


  Query Match             78.3%;  Score 18;  DB 21;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ildv 4


RESULT  18
AAY77431
ID   AAY77431 standard; peptide; 5 AA.
XX
AC   AAY77431;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Fibronectin CS1 peptidomimetic #22.
XX
KW   Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW   CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW   inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   5
FT                   /note= "C-terminal amide, D-form residue"
XX
PN   WO200002903-A1.
XX
PD   20-JAN-2000.
XX
PF   15-DEC-1998;   98WO-US26605.
XX
PR   10-JUL-1998;   98US-0113689.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Arrhenius TS,  Elices MJ,  Gaeta FCA,  He Y,  Huyghe BG,  Chen PG;
XX
DR   WPI; 2000-182213/16.
XX
PT   New peptidomimetic compounds used as cell surface fibronectin
PT   expressing receptor and VLA-4 inhibitors for treating inflammatory and
PT   cardiovascular disorders  -
XX
PS   Disclosure; Page 136; 243pp; English.
XX
CC   The invention relates to peptidomimetic compounds (AAY77415-Y77438)
CC   capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
CC   CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
CC   the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
CC   the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
CC   important role in the maturation and trafficking. VLA-4-mediated
CC   leukocyte adhesion to the CS-1 FN of endothelial cells is also a
CC   critical step in the inflammatory response. The peptidomimetics of the
CC   invention may be used to treat both chronic and acute immunoinflammatory
CC   conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
CC   allograft rejection. They may also be used to treat psoriasis and other
CC   skin inflammations, demyelinating diseases of the central nervous system
CC   (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
CC   diabetes, inflammatory bowel disease, kidney inflammation and
CC   restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
CC   involves the use of anti-VLA-4 antibodies, which can themselves induce an
CC   immune response on repeated administration, or the 25-mer CS-1 peptide,
CC   which is large and costly to make and is subject to rapid proteolytic
CC   degradation. The peptidomimetics of the invention are smaller in
CC   comparison to the CS-1 peptide and therefore less expensive to
CC   manufacture, and are resistant to proteolysis. Sequences AAY77415-Y77433
CC   represent specific examples of the inhibitory peptidomimetics of the
CC   invention.
XX
SQ   Sequence   5 AA;


  Query Match             78.3%;  Score 18;  DB 21;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ildv 4


RESULT  19
AAR92849
ID   AAR92849 standard; peptide; 5 AA.
XX
AC   AAR92849;
XX
DT   03-OCT-1996  (first entry)
XX
DE   Cell adhesion modulatory peptide AP21.
XX
KW   Intercellular adhesion; stimulation; inhibition; skin graft;
KW   synthetic blood vessel; coating; endothelial cell; epidermal cell;
KW   chemotactic attractor; wound healing; organ transplantation;
KW   thrombosis; arteriosclerosis; cancer metastases.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         3..5
FT                   /label= tripeptide
FT                   /note= "this tripeptide is also specifically
FT                          claimed"
XX
PN   DE4430601-A1.
XX
PD   29-FEB-1996.
XX
PF   22-AUG-1994;   94DE-4430601.
XX
PR   22-AUG-1994;   94DE-4430601.
XX
PA   (BEIE ) BEIERSDORF AG.
XX
PI   Doerschner A,  Eichner W,  Kock K,  Mielke H;
XX
DR   WPI; 1996-130242/14.
XX
PT   Peptide(s) that stimulate or inhibit cell to cell adhesion  - used
PT   e.g. to coat synthetic blood vessels with endothelial cells, to
PT   prepare, or increase growth of skin grafts, to prevent thrombosis
PT   etc.
XX
PS   Claim 9; Page 14; 18pp; German.
XX
CC   The present peptide is a specifically claimed example of a peptide
CC   which contains the highly generic sequence AA5-AA4-AA3-AA2-AA1-(AAX)n
CC   where AA5 is Glu, Ser, Asp or Asn; AA4 is Leu or Ser, AA3 is Leu, Ile,
CC   Phe or Gly; AA2 is Asp, Leu, Asn or Ser; AA1 is Gly, Pro or Asp; AAX
CC   is any amino acid and n = 0 or 1. When two or more such peptides are
CC   attached to a carrier, the product can be used for stimulating
CC   adhesion of eukaryotic cells in vitro. Particular applications include
CC   coating synthetic blood vessels with endothelial cells, preparing skin
CC   grafts using epithelial cells or stimulating wound healing. When a
CC   single peptide is used it may inhibit intercellular adhesion, making
CC   it useful for preventing thrombosis or arteriosclerosis or to suppress
CC   cancer metastases. The peptides can also be used as chemotactic
CC   attractors and for detecting/quantifying cell-cell adhesion in vitro.
```

```
XX
SQ   Sequence   5 AA;

  Query Match             73.9%;  Score 17;  DB 17;  Length 5;
  Best Local Similarity   75.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eild 4
          |:||
Db      1 elld 4


RESULT  20
AAR95707
ID   AAR95707 standard; peptide; 5 AA.
XX
AC   AAR95707;
XX
DT   03-DEC-1996  (first entry)
XX
DE   Alpha-4Beta-1 integrin binding inhibitory peptide 4.
XX
KW   VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW   inhibitor; binding; white blood cell; migration; capillary wall;
KW   tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW   CS1; CS5; H1; LDV; active site.
XX
OS   Synthetic.
XX
PN   US5510332-A.
XX
PD   23-APR-1996.
XX
PF   07-JUL-1994;   94US-0271830.
XX
PR   07-JUL-1994;   94US-0271830.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Beck PJ,  Kogan TP,  Ren K,  Vanderslice P;
XX
DR   WPI; 1996-221274/22.
XX
PT   New peptide(s) based on the LDV domain of fibronectin - used for
PT   inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT   fibronectin or invasin
XX
PS   Claim 2; Column 15; 35pp; English.
XX
CC   Vascular cell adhesion molecule-1 (VCAM-1) is  protein found on the
CC   surface of endothelial cells that line the interior wall of capillaries.
CC   VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC   VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC   surface of certain white blood cells.  Binding of IA4B1 to VCAM-1 allows
CC   white blood cells to adhere to the capillary wall in areas where the
CC   tissue surrounding the capillary has been infected or damaged. Sometimes
CC   this white blood cell migration can become uncontrolled, with white
CC   blood cells flooding to the scene, causing widespread tissue damage.
CC   Cpds. capable of blocking this process may be beneficial as therapeutic
CC   agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC   fibronectin. Three distinct IA4B1-binding sites have been identified
CC   within fibronectin. One site is found in the HeplI region and is
CC   expressed in all isoforms; two others (CS1 and CS5) are present in the
CC   alternatively spliced type III connecting segments.  CS1 has the higher
CC   affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC   site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC   peptide that include the LDV domain presented in such a way by its novel
CC   flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ   Sequence   5 AA;

  Query Match             69.6%;  Score 16;  DB 17;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          | |||
Db      1 ewldv 5


RESULT  21
AAR95716
ID   AAR95716 standard; peptide; 5 AA.
XX
AC   AAR95716;
XX
DT   04-DEC-1996  (first entry)
XX
DE   Alpha-4Beta-1 integrin binding inhibitory peptide 13.
XX
KW   VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW   inhibitor; binding; white blood cell; migration; capillary wall;
KW   tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW   CS1; CS5; H1; LDV; active site.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   10
FT                   /note= "Val-NH2"
XX
PN   US5510332-A.
XX
PD   23-APR-1996.
XX
PF   07-JUL-1994;   94US-0271830.
XX
PR   07-JUL-1994;   94US-0271830.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Beck PJ,  Kogan TP,  Ren K,  Vanderslice P;
XX
DR   WPI; 1996-221274/22.
XX
PT   New peptide(s) based on the LDV domain of fibronectin - used for
PT   inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT   fibronectin or invasin
XX
PS   Claim 4; Column 19-20; 35pp; English.
XX
CC   Vascular cell adhesion molecule-1 (VCAM-1) is  protein found on the
CC   surface of endothelial cells that line the interior wall of capillaries.
CC   VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC   VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC   surface of certain white blood cells.  Binding of IA4B1 to VCAM-1 allows
CC   white blood cells to adhere to the capillary wall in areas where the
CC   tissue surrounding the capillary has been infected or damaged. Sometimes
CC   this white blood cell migration can become uncontrolled, with white
CC   blood cells flooding to the scene, causing widespread tissue damage.
CC   Cpds. capable of blocking this process may be beneficial as therapeutic
CC   agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC   fibronectin. Three distinct IA4B1-binding sites have been identified
CC   within fibronectin. One site is found in the HeplI region and is
CC   expressed in all isoforms; two others (CS1 and CS5) are present in the
CC   alternatively spliced type III connecting segments.  CS1 has the higher
CC   affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC   site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC   peptide that include the LDV domain presented in such a way by its novel
CC   flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ   Sequence   5 AA;
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```
  Query Match            69.6%;  Score 16;  DB 17;  Length 5;
  Best Local Similarity  80.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          | |||
Db      1 ewldv 5


RESULT  22
AAR95717
ID   AAR95717 standard; peptide; 5 AA.
XX
AC   AAR95717;
XX
DT   04-DEC-1996  (first entry)
XX
DE   Alpha-4Beta-1 integrin binding inhibitory peptide 14.
XX
KW   VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW   inhibitor; binding; white blood cell; migration; capillary wall;
KW   tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW   CS1; CS5; H1; LDV; active site.
XX
OS   Synthetic.
XX
PN   US5510332-A.
XX
PD   23-APR-1996.
XX
PF   07-JUL-1994;   94US-0271830.
XX
PR   07-JUL-1994;   94US-0271830.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Beck PJ,  Kogan TP,  Ren K,  Vanderslice P;
XX
DR   WPI; 1996-221274/22.
XX
PT   New peptide(s) based on the LDV domain of fibronectin - used for
PT   inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT   fibronectin or invasin
XX
PS   Claim 4; Column 21-22; 35pp; English.
XX
CC   Vascular cell adhesion molecule-1 (VCAM-1) is  protein found on the
CC   surface of endothelial cells that line the interior wall of capillaries.
CC   VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC   VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC   surface of certain white blood cells.  Binding of IA4B1 to VCAM-1 allows
CC   white blood cells to adhere to the capillary wall in areas where the
CC   tissue surrounding the capillary has been infected or damaged. Sometimes
CC   this white blood cell migration can become uncontrolled, with white
CC   blood cells flooding to the scene, causing widespread tissue damage.
CC   Cpds. capable of blocking this process may be beneficial as therapeutic
CC   agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC   fibronectin. Three distinct IA4B1-binding sites have been identified
CC   within fibronectin. One site is found in the HeplI region and is
CC   expressed in all isoforms; two others (CS1 and CS5) are present in the
CC   alternatively spliced type III connecting segments.  CS1 has the higher
CC   affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC   site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC   peptide that include the LDV domain presented in such a way by its novel
CC   flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ   Sequence   5 AA;


  Query Match            69.6%;  Score 16;  DB 17;  Length 5;
  Best Local Similarity  80.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          | |||
Db      1 ewldv 5


RESULT  23
AAR99748
ID   AAR99748 standard; peptide; 5 AA.
XX
AC   AAR99748;
XX
DT   02-SEP-1996  (first entry)
XX
DE   Cyclic peptide inhibitor of alpha-4/beta-1 integrin binding to VCAM-1.
XX
KW   Vascular cell adhesion molecule 1; integrin; fibronectin; invasin;
KW   binding inhibitor; atherosclerosis; allergy; rheumatoid arthritis;
KW   asthma; multiple sclerosis; type 1 diabetes; cancer; cyclic;
KW   white blood cell; metastasis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "cross-link between Glu at position 1 and
FT                           Val at position 5"
FT   Modified-site   5
FT                   /note= "cross-link between Glu at position 1 and
FT                           Val at position 5"
XX
PN   WO9600581-A1.
XX
PD   11-JAN-1996.
XX
PF   27-JUN-1995;   95WO-US08353.
XX
PR   29-JUN-1994;   94US-0268192.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Beck PJ,  Kogan TP,  Ren K,  Vanderslice P;
XX
DR   WPI; 1996-077338/08.
XX
PT   Isolated, purified cyclic peptide which inhibits binding of alpha-4
PT   beta-1 integrin to VCAM-1 or fibronectin - useful for treating e.g.
PT   atherosclerosis or allergy
XX
PS   Claim 6; Page 27; 51pp; English.
XX
CC   AAR99746-R99785 are cyclic peptides which selectively inhibit binding
CC   of alpha4beta1 integrin to proteins such as vascular cell adhesion
CC   molecule 1 (VCAM-1), fibronectin and invasin. Due to this action the
CC   peptides are useful in pharmaceutical prepns. for the treatment of
CC   such ailments as asthma, atherosclerosis, rheumatoid arthritis,
CC   allergy, multiple sclerosis, type 1 diabetes and certain cancers
CC   (e.g. leukaemia, melanoma, lymphoma and sarcoma), as cell adhesion
CC   involving the alpha4beta1 integrin is believed to be involved in
CC   metastasis.
XX
SQ   Sequence   5 AA;


  Query Match            69.6%;  Score 16;  DB 17;  Length 5;
  Best Local Similarity  80.0%;  Pred. No. 6.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          | |||
Db      1 ewldv 5


RESULT  24
```

```
AAW45731
ID   AAW45731 standard; peptide; 5 AA.
XX
AC   AAW45731;
XX
DT   17-JUN-1998  (first entry)
XX
DE   Precursor peptide #2.
XX
KW   Cyclic peptide; dimeric peptide; vascular cell adhesion molecule-1;
KW   VCAM-1; fibronectin; integrin; rheumatoid arthritis; asthma;
KW   multiple sclerosis; VLA-4; very late antigen-4; precursor.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "D-form residue"
FT   Modified-site   3
FT                   /note= "Asp(OBut)"
FT   Modified-site   5
FT                   /note= "Piperazinyl-1-yl-acetic acid"
XX
PN   WO9702289-A1.
XX
PD   23-JAN-1997.
XX
PF   02-JUL-1996;   96WO-GB01580.
XX
PR   01-JUN-1996;   96GB-0011470.
PR   06-JUL-1995;   95GB-0013798.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Dutta AS;
XX
DR   WPI; 1997-108916/10.
XX
PT   Cyclic octa:peptide comprising dimeric tetra:peptides joined by two
PT   peptide mimetic linking gps. - block interaction of VCAM-1 and/or
PT   fibronectin with integrin VLA4, used in treating arthritis, asthma
PT   and multiple sclerosis
XX
PS   Example 1; Page 30; 82pp; English.
XX
CC   The present sequence represents a precursor peptide. The invention
CC   relates to cyclic peptides which block the interaction of protein
CC   ligand VCAM-1 (vascular cell adhesion molecule-1) to its integrin
CC   receptor VLA-4 (very late antigen-4), thereby modulating T-cell
CC   proliferation, B-cell localisation to germinal centres and adhesion of
CC   activated T-cells and eosinophils to endothelial cells. These peptides
CC   are thus of use in treating diseases associated with these processes,
CC   including rheumatoid arthritis, multiple sclerosis and asthma, melanoma
CC   cell invasion in metastasis, autoimmune diabetes, colitis, autoimmune
CC   encephalomyelitis, atherosclerosis, peripheral vascular or
CC   cardiovascular disease, nephritis, allograft rejection, psoriasis,
CC   restenosis, myocarditis, and inflammatory bowel disease.
XX
SQ   Sequence   5 AA;


  Query Match             69.6%;  Score 16;  DB 18;  Length 5;
  Best Local Similarity   75.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          :|||
Db      1 lldv 4


RESULT  25
AAY30308
ID   AAY30308 standard; peptide; 5 AA.
XX
AC   AAY30308;
XX
DT   23-NOV-1999  (first entry)
XX
DE   Angiopoietin derived peptide #23.
XX
KW   Angiogenesis; tumour; metastasis; wound healing; diabetic retinopathy;
KW   rheumatoid arthritis; psoriasis; cancer; blood supply; imaging;
KW   treatment; angiopoietin; Tie-1; Tie-2; TPCK Trypsin; protease;
KW   receptor tyrosine kinase.
XX
OS   Synthetic.
XX
PN   WO9940947-A2.
XX
PD   19-AUG-1999.
XX
PF   11-FEB-1999;   99WO-CA00101.
XX
PR   11-FEB-1998;   98US-0074420.
XX
PA   (RESO-) RESOLUTION PHARM INC.
XX
PI   Eshima D,  Fauconnier T,  Pollak A,  Thornback J;
XX
DR   WPI; 1999-527342/44.
XX
PT   Angiogenesis targeting molecules, for, e.g. detecting and treating
PT   cancer
XX
PS   Example 16; Page 50; 70pp; English.
XX
CC   Sequences AAY30286-Y30310 and AAY34151-Y34156 are peptides derived from
CC   the angiopoietins through cleavage by the proteases TPCK Trypsin or
CC   Staphylococcus aureus protease. The angiopoietins bind to the receptor
CC   tyrosine kinase Tie-2 which is upregulated during angiogenesis.
CC   Angiopoietin 1 (Ang 1) is ubiquitously expressed and interacts with
CC   Tie-2 on endothelial cells and early haemopoietic cells. Angiopoietin 2
CC   (Ang 2) is homologous to Ang 1 and competitively inhibits Ang 1
CC   interaction with Tie-2. Angiogenesis is the process involved in creating
CC   a blood supply to a tumour. The peptides are used in a compound that
CC   binds to sites of angiogenesis. The compound consists of a chelator
CC   moiety capable of complexing a radionuclide metal or a moiety capable of
CC   binding to a halogen group, and an angiogenesis targeting molecule. The
CC   peptides are incorporated in the angiogenesis targeting molecule. The
CC   compounds are used for imaging and treating angiogenesis, and also to
CC   detect, stage and treat tumours and metastases. Angiogenesis is also
CC   required for wound healing and conditions such as diabetic retinopathy,
CC   rheumatoid arthritis and psoriasis, therefore the compounds may also be
CC   useful in the treatment of these conditions.
XX
SQ   Sequence   5 AA;


  Query Match             69.6%;  Score 16;  DB 20;  Length 5;
  Best Local Similarity   75.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eild 4
          :|||
Db      2 qild 5


RESULT  26
AAR82907
ID   AAR82907 standard; peptide; 3 AA.
XX
AC   AAR82907;
XX
DT   20-DEC-1995  (first entry)
XX
DE   Non-RGD, non-YISGR cancer metastasis inhibitory peptide #1.
```

XX
KW Cancer metastasis; adhesive peptide; core sequence; dextran; cancer;
KW water soluble polysaccharide; metastasis; wound; immunogenicity.
XX
OS Synthetic.
XX
PN JP07089999-A.
XX
PD 04-APR-1995.
XX
PF 17-SEP-1993; 93JP-0254779.
XX
PR 17-SEP-1993; 93JP-0254779.
XX
PA (JAPG) NIPPON ZEON KK.
XX
DR WPI; 1995-167254/22.
XX
PT Cancer metastasis inhibitive peptide derivs. - useful for inhibition
PT of cancer metastasis, healing of wounds and regulation of
PT immunogenicity.
XX
PS Disclosure; Page 3; 6pp; Japanese.
XX
CC The peptides AAR70472-90 and AAR82907-24 are peptide derivatives which
CC inhibit cancer metastasis. They are composed of an adhesive peptide
CC with a core sequence selected from: RGD (AAR70472-85), YIGSR
CC (AAR70486-90) or other sequence (AAR82907-24), linked to a water soluble
CC polysaccharide, preferably a water soluble dextran, at the C-terminus.
CC The peptides are useful in inhibiting cancer metastasis, healing wounds
CC and the regulation of immunogenicity.
XX
SQ Sequence 3 AA;

Query Match 60.9%; Score 14; DB 16; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ldv 5
|||
Db 1 ldv 3

RESULT 27
AAW25187
ID AAW25187 standard; peptide; 3 AA.
XX
AC AAW25187;
XX
DT 05-JAN-1998 (first entry)
XX
DE LDV-peptide capable of binding cell adhesion molecules.
XX
KW LDV; leucine; aspartic acid; valine; cell adhesion molecule;
KW binding; bladder irrigation; tumour removal; endoscopic operation;
KW transurethral resection; cancer; neoplasia.
XX
OS Synthetic.
XX
PN DE19529909-A1.
XX
PD 20-FEB-1997.
XX
PF 15-AUG-1995; 95DE-1029909.
XX
PR 15-AUG-1995; 95DE-1029909.
XX
PA (FREP) FRESENIUS AG.
XX
PI Boehle A;
XX
DR WPI; 1997-133793/13.
XX
PT Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
PT adhesion molecules
XX
PS Claim 6; Page 8; 8pp; German.
XX
CC AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
CC The peptides are capable of binding to cell adhesion molecules and
CC are used in aqueous irrigation solutions for use during and after
CC endoscopic operations. Preferred irrigation solutions are
CC electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
CC oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
CC GPRP, VTL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid
CC code). The solutions are especially used for irrigating the bladder
CC during and after tumour removal by transurethral resection. The
CC peptides protect against recurrence of tumours.
XX
SQ Sequence 3 AA;

Query Match 60.9%; Score 14; DB 18; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ldv 5
|||
Db 1 ldv 3

RESULT 28
AAB01568
ID AAB01568 standard; peptide; 3 AA.
XX
AC AAB01568;
XX
DT 08-NOV-2000 (first entry)
XX
DE Cell binding domain of Fibronectin.
XX
KW Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;
KW sealant; tissue engineering; wound healing; scaffold;
KW cell transplant; adhesion prevention; cell migration; collagenase;
KW plasmin; elastase.
XX
OS Synthetic.
XX
PN WO200044808-A1.
XX
PD 03-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US02608.
XX
PR 01-FEB-1999; 99US-0118093.
XX
PA (HUBB/) HUBBELL J A.
XX
PI Hubbell JA, Elbert D, Lutolf M, Pratt A, Schoenmakers R;
PI Tirelli N, Vernon B;
XX
DR WPI; 2000-524289/47.
XX
PT Producing polymeric biomaterials by polymerizing two or more precursor
PT components (e.g. polymer, protein or peptide) of the biomaterial,
PT useful for delivering therapeutic molecules to a subject and as
PT adhesives or sealants
XX
PS Disclosure; Page 52; 119pp; English.
XX
CC A method of making polymeric biomaterials is described comprising
CC combining two or more precursor components (e.g. polymer, protein or
CC peptide) of the biomaterial under conditions that allow
CC polymerisation of the two components. Polymerisation occurs through
CC self selective reaction between a strong nucleophile and a conjugated

CC unsaturated bond or a conjugated unsaturated group, by nucleophilic
CC addition. The polymeric hydrogels can be used in a variety of
CC applications. They can be used to deliver therapeutic molecules to
CC a subject, as adhesives or sealants (e.g. sealing air leaks on the
CC lung), as tissue engineering and wound healing scaffolds, and as cell
CC transplant devices. The biomaterials are also useful for adhesion
CC prevention to minimise unwanted operative or post-traumatic adhesions.
CC A variety of adhesion-promoting peptides have been identified as
CC being the active domains of adhesion-promoting proteins such as
CC fibronectin, vitronectin, laminin, collagen, von Willebrand factor
CC osteonectin etc.. These peptides can be incorporated into the
CC biomaterial when they are designed with a strong nucleophile in the
CC peptide chain such as cysteine. These peptides are potentially useful
CC in controlling a variety of cellular reactions such as cell
CC attachment, migration and overgrowth on a material surface when the
CC material is non bio-degradable or slowly degradable, and cell
CC migration through a material when that material is biodegradable.
CC The peptides are also useful in the induction of particular cellular
CC phenotypes.
XX
SQ Sequence 3 AA;

Query Match 60.9%; Score 14; DB 21; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ldv 5
|||
Db 1 ldv 3

RESULT 29
AAB91984
ID AAB91984 standard; Peptide; 3 AA.
XX
AC AAB91984;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1160.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
PS Disclosure; Page 574; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 3 AA;

Query Match 60.9%; Score 14; DB 22; Length 3;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ldv 5
|||
Db 1 ldv 3

RESULT 30
AAP91609
ID AAP91609 standard; protein; 4 AA.
XX
AC AAP91609;
XX
DT 09-JUL-1990 (first entry)
XX
DE Motif useful in tolerization alone or in association with epitopes to
DE myelin basic protein.
XX
KW Autoantigen; MBP; myelin basic protein; transplantation antigen;
KW myasthenia gravis; myasthenics; Transplantation antigen.
XX
OS Synthetic.
XX
PN EP304279-A.
XX
PD 22-FEB-1989.
XX
PF 17-AUG-1988; 88EP-0307608.
XX
PR 17-AUG-1988; 88US-0086694.
XX
PA (STRD) LELAND STANFORD JR UNIV.
XX
PI Steinman L;
XX
DR WPI; 1989-055696/08.
XX
PT Oligopeptide and polypeptide compsns. -
PT based on the amino acid sequence of an immunogen and used for
PT modulating the immune system.
XX
PS Disclosure; ; 7pp; English.
XX
CC Sequences will normally be part of 9-15 amino acid sequence, excluded as
CC motifs for immunisation but useful in tolerisation..
XX
SQ Sequence 4 AA;

Query Match 60.9%; Score 14; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 ild 4
          |||
Db      2 ild 4


RESULT  31
AAW01711
ID   AAW01711 standard; peptide; 4 AA.
XX
AC   AAW01711;
XX
DT   16-APR-1997  (first entry)
XX
DE   Inhibitor of fibronectin CS-1 peptide and VLA-4 receptor binding.
XX
KW   fibronectin; high affinity; CS-1; recognition sequence; VLA-4;
KW   alpha-4 beta-1 cell adhesion receptor; CD49d/CD29; inhibitor;
KW   leukocyte trafficking function; peptidomimetic; treatment; asthma;
KW   rheumatoid arthritis; osteoarthritis; allograft rejection;
KW   skin inflammation; central nervous system demyelinating disease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "when D-form Pro at position 4, Leu is
FT                          modified by: phthalimido, phenylacetyl,
FT                          pyridine-3-carbonyl, benzoyl, phenylpropionyl,
FT                          2,3-dimethylbenzoyl, 3,4-dimethylbenzoyl,
FT                          pyridine-2-carbonyl, cyclohexanecarbonyl,
FT                          2,5-dimethylbenzoyl, 3-methylvaleroyl,
FT                          4-methylvaleroyl, cyclohexaneacetyl, 1-naphthoyl,
FT                          cyclohexanepropionyl, adamantanecarbonyl,
FT                          2-naphthoyl, cinnamoyl; when L-Pro at residue 4,
FT                          Leu is modified by benzoyl or pivaloyl"
FT   Modified-site   4
FT                   /note= "Pro-NH2, optionally D-form residue"
XX
PN   WO9515973-A1.
XX
PD   15-JUN-1995.
XX
PF   05-DEC-1994;   94WO-US13943.
XX
PR   02-DEC-1994;   94US-0164101.
PR   06-DEC-1993;   93US-0164101.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Arrhenius TS,  Elices MJ,  Gaeta FCA;
XX
DR   WPI; 1995-224284/29.
XX
PT   New peptide mimics of fibronectin CS-1 sequence - inhibit
PT   interaction of endothelial cells and VLA-4 carrying inflammatory
PT   cells, for treating or preventing asthma, arthritis etc.
XX
PS   Disclosure; Page 33-37; 103pp; English.
XX
CC   The alpha-4 beta-1 (CD49d/CD29, VLA-4) cell adhesion receptor is an
CC   active participant in leukocyte trafficking functions. Binding of
CC   inflammatory cells to endothelial cells that express the CS-1 portion
CC   (AAW01703) of fibronectin on their surfaces can be inhibited by CS-1
CC   peptidomimetic cpds. of minimal length. A minimal essential sequence for
CC   specific VLA-4 recognition of CS-1 has been identified as the tripeptide
CC   LDV. A generic peptidomimetic inhibits the binding of Jurkat cells
CC   (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay
CC   in an aq. buffer at a pH value of 7.2-7.4 to an extent that is equal to
CC   or upto about 3000-fold greater than the inhibition in the binding
CC   exhibited by AAW01705. CS-1 mediated inflammation, e.g. asthma,
CC   rheumatoid arthritis, osteoarthritis, allograft rejection, skin
CC   inflammation or central nervous system demyelinating disease, can be
CC   treated by the peptidomimetics. AAW01706-27 are exemplary inhibitor
CC   peptides.
XX
SQ   Sequence   4 AA;


  Query Match             60.9%;  Score 14;  DB 16;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 ldv 5
          |||
Db      1 ldv 3


RESULT  32
AAR66483
ID   AAR66483 standard; Protein; 4 AA.
XX
AC   AAR66483;
XX
DT   05-AUG-1995  (first entry)
XX
DE   Sodium channel gene, alpha subunit domain IV, segment 53.
XX
KW   Hyperkalemic periodic paralysis; quarter horse; sodium channel;
KW   prenatal diagnosis.
XX
OS   Equus caballus.
XX
PN   US5356777-A.
XX
PD   18-OCT-1994.
XX
PF   01-OCT-1992;   92US-0954830.
XX
PR   01-OCT-1992;   92US-0954830.
XX
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Bernoco D,  Byrns G,  Hoffman EP,  Rudolph JA,  Spier SJ;
XX
DR   WPI; 1995-013469/02.
DR   N-PSDB; AAQ75256.
XX
PT   Detecting hyperkalaemic periodic paralysis in horses - by
PT   identifying a single base mutation in the skeletal muscle sodium
PT   channel gene, can be used for prenatal diagnosis.
XX
PS   Disclosure; Column 19; 15pp; English.
XX
CC   Single strand conformation polymorphism analysis revealed a
CC   conformer in the sodium channel gene, domain IV, segment 53,
CC   in horses affected by hyperkalemic periodic paralysis.  A C to G
CC   transversion (AAQ75256) was present in 5/18 sequenced clones from
CC   the horse.  The sequence found in unaffected horses is given in
CC   AAQ75255.
XX
SQ   Sequence   4 AA;


  Query Match             60.9%;  Score 14;  DB 16;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ild 4
          |||
Db      1 ild 3


RESULT  33
AAR95728
ID   AAR95728 standard; peptide; 4 AA.
```

```
XX
AC   AAR95728;
XX
DT   04-DEC-1996  (first entry)
XX
DE   Alpha-4Beta-1 integrin binding inhibitory peptide 25.
XX
KW   VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW   inhibitor; binding; white blood cell; migration; capillary wall;
KW   tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW   CS1; CS5; H1; LDV; active site.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "Val-NH2"
XX
PN   US5510332-A.
XX
PD   23-APR-1996.
XX
PF   07-JUL-1994;   94US-0271830.
XX
PR   07-JUL-1994;   94US-0271830.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Beck PJ,  Kogan TP,  Ren K,  Vanderslice P;
XX
DR   WPI; 1996-221274/22.
XX
PT   New peptide(s) based on the LDV domain of fibronectin - used for
PT   inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT   fibronectin or invasin
XX
PS   Claim 4; Column 27-28; 35pp; English.
XX
CC   Vascular cell adhesion molecule-1 (VCAM-1) is  protein found on the
CC   surface of endothelial cells that line the interior wall of capillaries.
CC   VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC   VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC   surface of certain white blood cells.  Binding of IA4B1 to VCAM-1 allows
CC   white blood cells to adhere to the capillary wall in areas where the
CC   tissue surrounding the capillary has been infected or damaged. Sometimes
CC   this white blood cell migration can become uncontrolled, with white
CC   blood cells flooding to the scene, causing widespread tissue damage.
CC   Cpds. capable of blocking this process may be beneficial as therapeutic
CC   agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC   fibronectin. Three distinct IA4B1-binding sites have been identified
CC   within fibronectin. One site is found in the HeplI region and is
CC   expressed in all isoforms; two others (CS1 and CS5) are present in the
CC   alternatively spliced type III connecting segments.  CS1 has the higher
CC   affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC   site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC   peptide that include the LDV domain presented in such a way by its novel
CC   flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ   Sequence   4 AA;

  Query Match          60.9%;  Score 14;  DB 17;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 ldv 5
          |||
Db      2 ldv 4


RESULT  34
AAR95731
ID   AAR95731 standard; peptide; 4 AA.
XX
AC   AAR95731;
XX
DT   04-DEC-1996  (first entry)
XX
DE   Alpha-4Beta-1 integrin binding inhibitory peptide 28.
XX
KW   VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW   inhibitor; binding; white blood cell; migration; capillary wall;
KW   tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW   CS1; CS5; H1; LDV; active site.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "Val-NH2"
XX
PN   US5510332-A.
XX
PD   23-APR-1996.
XX
PF   07-JUL-1994;   94US-0271830.
XX
PR   07-JUL-1994;   94US-0271830.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Beck PJ,  Kogan TP,  Ren K,  Vanderslice P;
XX
DR   WPI; 1996-221274/22.
XX
PT   New peptide(s) based on the LDV domain of fibronectin - used for
PT   inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT   fibronectin or invasin
XX
PS   Claim 4; Column 27-28; 35pp; English.
XX
CC   Vascular cell adhesion molecule-1 (VCAM-1) is  protein found on the
CC   surface of endothelial cells that line the interior wall of capillaries.
CC   VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC   VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC   surface of certain white blood cells.  Binding of IA4B1 to VCAM-1 allows
CC   white blood cells to adhere to the capillary wall in areas where the
CC   tissue surrounding the capillary has been infected or damaged. Sometimes
CC   this white blood cell migration can become uncontrolled, with white
CC   blood cells flooding to the scene, causing widespread tissue damage.
CC   Cpds. capable of blocking this process may be beneficial as therapeutic
CC   agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC   fibronectin. Three distinct IA4B1-binding sites have been identified
CC   within fibronectin. One site is found in the HeplI region and is
CC   expressed in all isoforms; two others (CS1 and CS5) are present in the
CC   alternatively spliced type III connecting segments.  CS1 has the higher
CC   affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC   site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC   peptide that include the LDV domain presented in such a way by its novel
CC   flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ   Sequence   4 AA;

  Query Match          60.9%;  Score 14;  DB 17;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 ldv 5
          |||
Db      2 ldv 4


RESULT  35
AAR95726
ID   AAR95726 standard; peptide; 4 AA.
```

```
XX
AC   AAR95726;
XX
DT   04-DEC-1996  (first entry)
XX
DE   Alpha-4Beta-1 integrin binding inhibitory peptide 23.
XX
KW   VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW   inhibitor; binding; white blood cell; migration; capillary wall;
KW   tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW   CS1; CS5; H1; LDV; active site.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Ac-Phe"
FT   Modified-site   4
FT                   /note= "Val-NH2"
XX
PN   US5510332-A.
XX
PD   23-APR-1996.
XX
PF   07-JUL-1994;   94US-0271830.
XX
PR   07-JUL-1994;   94US-0271830.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Beck PJ,  Kogan TP,  Ren K,  Vanderslice P;
XX
DR   WPI; 1996-221274/22.
XX
PT   New peptide(s) based on the LDV domain of fibronectin - used for
PT   inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
PT   fibronectin or invasin
XX
PS   Claim 4; Column 25-26; 35pp; English.
XX
CC   Vascular cell adhesion molecule-1 (VCAM-1) is  protein found on the
CC   surface of endothelial cells that line the interior wall of capillaries.
CC   VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
CC   VLA-4 for very late antigen-4), a heterodimeric protein present on the
CC   surface of certain white blood cells.  Binding of IA4B1 to VCAM-1 allows
CC   white blood cells to adhere to the capillary wall in areas where the
CC   tissue surrounding the capillary has been infected or damaged. Sometimes
CC   this white blood cell migration can become uncontrolled, with white
CC   blood cells flooding to the scene, causing widespread tissue damage.
CC   Cpds. capable of blocking this process may be beneficial as therapeutic
CC   agents. IA4B1 also recognises the extracellular matrix glycoprotein
CC   fibronectin. Three distinct IA4B1-binding sites have been identified
CC   within fibronectin. One site is found in the HeplI region and is
CC   expressed in all isoforms; two others (CS1 and CS5) are present in the
CC   alternatively spliced type III connecting segments.  CS1 has the higher
CC   affinity for IA4B1 and contains the tripeptide LDV as its minimal active
CC   site. Peptides AAR95704-805 are modeled after a portion of the CS1
CC   peptide that include the LDV domain presented in such a way by its novel
CC   flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ   Sequence   4 AA;


  Query Match             60.9%;  Score 14;  DB 17;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 ldv 5
           |||
Db       2 ldv 4
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Job time: 241 sec

OM protein - protein search, using sw model

Run on: June 10, 2002, 06:36:37 ; Search time 15.68 Seconds
(without alignments)
7.789 Million cell updates/sec

Title: 09-251073
Perfect score: 23
Sequence: 1 eildv 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 17877

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	23	100.0	5	1	US-08-109-106-3	Sequence 3, Appli
2	23	100.0	5	1	US-08-303-162A-3	Sequence 3, Appli
3	23	100.0	5	1	US-08-634-060-3	Sequence 3, Appli
4	23	100.0	5	1	US-08-338-282-10	Sequence 10, Appl
5	23	100.0	5	1	US-08-709-515-3	Sequence 3, Appli
6	23	100.0	5	2	US-08-700-846-2	Sequence 2, Appli
7	23	100.0	5	4	US-09-146-503-3	Sequence 3, Appli
8	23	100.0	5	4	US-08-983-391-2	Sequence 2, Appli
9	23	100.0	5	4	US-08-498-237-2	Sequence 2, Appli
10	23	100.0	5	4	US-08-376-372-2	Sequence 2, Appli
11	23	100.0	5	5	PCT-US95-07542-3	Sequence 3, Appli
12	19	82.6	5	1	US-08-271-830-16	Sequence 16, Appl
13	19	82.6	5	3	US-08-860-248C-39	Sequence 39, Appl
14	19	82.6	5	3	US-09-059-111-8	Sequence 8, Appli
15	19	82.6	5	5	PCT-US95-08353-8	Sequence 8, Appli
16	18	78.3	5	1	US-08-435-286-13	Sequence 13, Appl
17	18	78.3	5	1	US-08-435-286-14	Sequence 14, Appl
18	18	78.3	5	3	US-08-860-248C-1	Sequence 1, Appli
19	18	78.3	5	3	US-08-860-248C-2	Sequence 2, Appli
20	18	78.3	5	3	US-08-860-248C-3	Sequence 3, Appli
21	18	78.3	5	3	US-08-860-248C-4	Sequence 4, Appli
22	18	78.3	5	3	US-08-860-248C-5	Sequence 5, Appli
23	18	78.3	5	3	US-08-860-248C-11	Sequence 11, Appl
24	18	78.3	5	3	US-08-860-248C-12	Sequence 12, Appl
25	18	78.3	5	3	US-08-860-248C-13	Sequence 13, Appl
26	18	78.3	5	3	US-08-860-248C-14	Sequence 14, Appl
27	18	78.3	5	3	US-08-860-248C-15	Sequence 15, Appl
28	18	78.3	5	3	US-08-860-248C-16	Sequence 16, Appl
29	18	78.3	5	3	US-08-860-248C-20	Sequence 20, Appl
30	18	78.3	5	3	US-08-860-248C-21	Sequence 21, Appl
31	18	78.3	5	3	US-08-860-248C-22	Sequence 22, Appl
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33	18	78.3	5	3	US-08-860-248C-24	Sequence 24, Appl
34	18	78.3	5	3	US-08-860-248C-25	Sequence 25, Appl
35	18	78.3	5	3	US-08-860-248C-26	Sequence 26, Appl
36	18	78.3	5	3	US-08-860-248C-28	Sequence 28, Appl
37	18	78.3	5	3	US-08-860-248C-35	Sequence 35, Appl
38	18	78.3	5	3	US-08-860-248C-40	Sequence 40, Appl
39	18	78.3	5	3	US-08-860-248C-41	Sequence 41, Appl
40	18	78.3	5	3	US-08-860-248C-42	Sequence 42, Appl
41	18	78.3	5	3	US-08-860-248C-43	Sequence 43, Appl
42	18	78.3	5	3	US-08-860-248C-55	Sequence 55, Appl
43	18	78.3	5	3	US-08-860-248C-58	Sequence 58, Appl
44	18	78.3	5	3	US-08-860-248C-70	Sequence 70, Appl
45	18	78.3	5	3	US-08-923-026-13	Sequence 13, Appl
46	18	78.3	5	3	US-08-923-026-14	Sequence 14, Appl
47	18	78.3	5	3	US-08-837-154-13	Sequence 13, Appl
48	18	78.3	5	3	US-08-837-154-14	Sequence 14, Appl
49	18	78.3	5	5	PCT-US94-13943-13	Sequence 13, Appl
50	18	78.3	5	5	PCT-US94-13943-14	Sequence 14, Appl
51	17	73.9	5	3	US-08-860-248C-30	Sequence 30, Appl
52	16	69.6	5	1	US-08-271-830-4	Sequence 4, Appli
53	16	69.6	5	3	US-08-860-248C-6	Sequence 6, Appli
54	16	69.6	5	3	US-08-860-248C-17	Sequence 17, Appl
55	16	69.6	5	3	US-08-860-248C-27	Sequence 27, Appl
56	16	69.6	5	3	US-08-860-248C-29	Sequence 29, Appl
57	16	69.6	5	3	US-08-860-248C-34	Sequence 34, Appl
58	16	69.6	5	3	US-08-860-248C-44	Sequence 44, Appl
59	16	69.6	5	3	US-08-860-248C-45	Sequence 45, Appl
60	16	69.6	5	3	US-08-860-248C-46	Sequence 46, Appl
61	16	69.6	5	3	US-08-860-248C-47	Sequence 47, Appl
62	16	69.6	5	3	US-08-860-248C-48	Sequence 48, Appl
63	16	69.6	5	3	US-08-860-248C-49	Sequence 49, Appl
64	16	69.6	5	3	US-08-860-248C-54	Sequence 54, Appl
65	16	69.6	5	3	US-08-860-248C-57	Sequence 57, Appl
66	16	69.6	5	3	US-08-860-248C-82	Sequence 82, Appl
67	16	69.6	5	3	US-08-860-248C-83	Sequence 83, Appl
68	16	69.6	5	3	US-08-860-248C-84	Sequence 84, Appl
69	16	69.6	5	3	US-09-059-111-4	Sequence 4, Appli
70	16	69.6	5	4	US-09-236-160-35	Sequence 35, Appl
71	16	69.6	5	5	PCT-US95-08353-4	Sequence 4, Appli
72	15	65.2	5	3	US-08-860-248C-36	Sequence 36, Appl
73	15	65.2	5	3	US-08-860-248C-69	Sequence 69, Appl
74	14	60.9	3	1	US-08-634-060-36	Sequence 36, Appl
75	14	60.9	3	1	US-08-338-282-11	Sequence 11, Appl
76	14	60.9	3	2	US-08-934-222-12	Sequence 12, Appl
77	14	60.9	3	2	US-08-933-402-12	Sequence 12, Appl
78	14	60.9	3	2	US-09-207-621-12	Sequence 12, Appl
79	14	60.9	3	2	US-08-532-818-12	Sequence 12, Appl
80	14	60.9	3	3	US-09-231-797-12	Sequence 12, Appl
81	14	60.9	3	3	US-09-086-421-1	Sequence 1, Appli
82	14	60.9	3	3	US-08-934-224-12	Sequence 12, Appl
83	14	60.9	3	3	US-08-933-843-12	Sequence 12, Appl
84	14	60.9	3	4	US-08-934-223-12	Sequence 12, Appl
85	14	60.9	3	4	US-09-413-492-12	Sequence 12, Appl
86	14	60.9	4	1	US-07-954-830-8	Sequence 8, Appli
87	14	60.9	4	1	US-08-271-830-1	Sequence 1, Appli
88	14	60.9	5	1	US-07-723-418-4	Sequence 4, Appli
89	14	60.9	5	1	US-08-271-830-5	Sequence 5, Appli
90	14	60.9	5	1	US-08-435-286-11	Sequence 11, Appl
91	14	60.9	5	2	US-08-483-077C-27	Sequence 27, Appl
92	14	60.9	5	2	US-08-465-380-74	Sequence 74, Appl
93	14	60.9	5	2	US-08-486-397-74	Sequence 74, Appl
94	14	60.9	5	2	US-08-486-399-74	Sequence 74, Appl
95	14	60.9	5	2	US-08-519-109B-27	Sequence 27, Appl
96	14	60.9	5	2	US-08-461-965-74	Sequence 74, Appl
97	14	60.9	5	2	US-08-634-641-74	Sequence 74, Appl
98	14	60.9	5	3	US-08-860-248C-7	Sequence 7, Appli
99	14	60.9	5	3	US-08-860-248C-8	Sequence 8, Appli
100	14	60.9	5	3	US-08-860-248C-9	Sequence 9, Appli

ALIGNMENTS

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RESULT  1
US-08-109-106-3
; Sequence 3, Application US/08109106
; Patent No. 5475100
;  GENERAL INFORMATION:
;    APPLICANT:  Kimikazu HASHINO et al.
;    TITLE OF INVENTION:  Artificial Antibody
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  DisplayWrite
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/109,106
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/725,668
;      FILING DATE:  July 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:  202-371-8856
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-109-106-3


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  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db       1 EILDV 5


RESULT  2
US-08-303-162A-3
; Sequence 3, Application US/08303162A
; Patent No. 5559099
;  GENERAL INFORMATION:
;    APPLICANT:  Wickham, Thomas J.
;    APPLICANT:  Kovesdi, Imre
;    APPLICANT:  Brough, Douglas E.
;    APPLICANT:  McVey, Duncan L.
;    APPLICANT:  Bruder, Joseph T.
;    TITLE OF INVENTION:  CHIMERIC PENTON BASE MOLECULES
;    TITLE OF INVENTION:  AND METHODS OF USING SAME
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,162A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kilyk, John Jr.
;      REGISTRATION NUMBER:  30763
;      REFERENCE/DOCKET NUMBER:  61306
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 616-5600
;      TELEFAX:  (312) 616-5700
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-303-162A-3


  Query Match           100.0%;  Score 23;  DB 1;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 eildv 5
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Db      1 EILDV 5


RESULT   3
US-08-634-060-3
; Sequence 3, Application US/08634060
; Patent No. 5712136
;  GENERAL INFORMATION:
;    APPLICANT:  Wickham, Thomas J.
;    APPLICANT:  Kovesdi, Imre
;    APPLICANT:  Roelvink, Petrus W.
;    TITLE OF INVENTION:  ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY
;    TITLE OF INVENTION:  THE ADENOVIRUS PENTON BASE PROTEIN
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/634,060
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/303,162
;      FILING DATE:  08-SEP-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kilyk, John Jr.
;      REGISTRATION NUMBER:  30763
;      REFERENCE/DOCKET NUMBER:  71602
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 616-5600
;      TELEFAX:  (312) 616-5700
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-634-060-3


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  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 EILDV 5


RESULT   4
US-08-338-282-10
; Sequence 10, Application US/08338282
; Patent No. 5730978
;  GENERAL INFORMATION:
;    APPLICANT:  Wayner, E.A.
;    TITLE OF INVENTION:  INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson and Kindness
;      STREET:  2800 Pacific First Center, 1420 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette-5.25 inch, 1.2Mb storage
;      COMPUTER:  IBM PC/386 Compatible
;      OPERATING SYSTEM:  MS-DOS 4.01
;      SOFTWARE:  Word for Windows-t
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/338,282
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/814,873
;      FILING DATE:  December 24, 1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/402,389
;      FILING DATE:  September 1, 1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sundsmo,John,S.
;      REGISTRATION NUMBER:  34,446
;      REFERENCE/DOCKET NUMBER:  CYTE-1-6162
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-206-682-8100; 1-206-224-0727 (direct)
;      TELEFAX:  1-206-224-0779
;      TELEX:  4938023
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;      DESCRIPTION:  EILDV
US-08-338-282-10


  Query Match             100.0%;  Score 23;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 EILDV 5


RESULT   5
US-08-709-515-3
; Sequence 3, Application US/08709515
; Patent No. 5731190
;  GENERAL INFORMATION:
;    APPLICANT:  Wickham, Thomas J.
;    APPLICANT:  Kovesdi, Imre
;    APPLICANT:  Brough, Douglas E.
;    APPLICANT:  McVey, Duncan L.
;    APPLICANT:  Bruder, Joseph T.
;    TITLE OF INVENTION:  CHIMERIC PENTON BASE MOLECULES
;    TITLE OF INVENTION:  AND METHODS OF USING SAME
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,515
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;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/303,162
;      FILING DATE:  08-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kilyk, John Jr.
;      REGISTRATION NUMBER:  30763
;      REFERENCE/DOCKET NUMBER:  73845
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 616-5600
;      TELEFAX:  (312) 616-5700
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-709-515-3


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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 EILDV 5


RESULT   6
US-08-700-846-2
; Sequence 2, Application US/08700846
; Patent No. 5962311
;  GENERAL INFORMATION:
;    APPLICANT:  WICKHAM, THOMAS J.
;    APPLICANT:  ROELVINK, PETRUS W.
;    APPLICANT:  KOVESDI, IMRE
;    TITLE OF INVENTION:  A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
;    TITLE OF INVENTION:  USE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LEYDIG, VOIT & MAYER, LTD.
;      STREET:  TWO PRUDENTIAL PLAZA, SUITE 4900
;      CITY:  CHICAGO
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,846
;      FILING DATE:  21-AUG-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LARCHER, CAROL
;      REGISTRATION NUMBER:  35243
;      REFERENCE/DOCKET NUMBER:  74294
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 616-5600
;      TELEFAX:  (312) 616-5700
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-700-846-2


  Query Match             100.0%;  Score 23;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 EILDV 5


RESULT   7
US-09-146-503-3
; Sequence 3, Application US/09146503
; Patent No. 6184206
; GENERAL INFORMATION:
;  APPLICANT: Jeffrey W. Smith
;  APPLICANT: Dana D. Hu
;  TITLE OF INVENTION: Integrin Ligand Dissociators
;  FILE REFERENCE: 02046.0002
;  CURRENT APPLICATION NUMBER: US/09/146,503
;  CURRENT FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: 60/057,463
;  EARLIER FILING DATE: 1997-09-03
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-146-503-3


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Qy      1 eildv 5
          |||||
Db      1 EILDV 5


RESULT   8
US-08-983-391-2
; Sequence 2, Application US/08983391
; Patent No. 6239108
; GENERAL INFORMATION:
;  APPLICANT:  Lin, Ko-Chung
;  APPLICANT:  Adams, Steven P.
;  APPLICANT:  Castro, Alfredo C.
;  APPLICANT:  Zimmerman, Craig N.
;  APPLICANT:  Cuervo, Julio Herman
;  APPLICANT:  Lee, Wen-Cherng
;  APPLICANT:  Hammond, Charles E.
;  APPLICANT:  Carter, Mary Beth
;  APPLICANT:  Almquist, Ronald G.
;  APPLICANT:  Ensinger, Carol Lee
;  TITLE OF INVENTION:  CELL ADHESION INHIBITORS
;  FILE REFERENCE:  10274/024002
;  CURRENT APPLICATION NUMBER: US/08/983,391
;  CURRENT FILING DATE:  1998-08-10
;  PRIOR APPLICATION NUMBER:  US 96/11570
;  PRIOR FILING DATE:  1996-07-11
;  PRIOR APPLICATION NUMBER:  US 08/498,237
;  PRIOR FILING DATE:  1995-07-11
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Synthetically generated protein
US-08-983-391-2


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Qy      1 eildv 5
          |||||
Db      1 EILDV 5


RESULT   9
US-08-498-237-2
; Sequence 2, Application US/08498237
; Patent No. 6248713
;  GENERAL INFORMATION:
;    APPLICANT:  Lin, Ko-Chung
;    APPLICANT:  Adams, Steven P
;    APPLICANT:  Castro, Alfredo C
;    APPLICANT:  Zimmerman, Craig N
;    APPLICANT:  Cuervo, Julio H
;    APPLICANT:  Lee, Wen-Cherng
;    APPLICANT:  Hammond, Charles E
;    APPLICANT:  Carter, Mary B
;    APPLICANT:  Almquist, Ronald G
;    TITLE OF INVENTION:  CELL ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/498,237
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr, James F
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B190
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-498-237-2


  Query Match           100.0%;  Score 23;  DB 4;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
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Db      1 EILDV 5


RESULT  10
US-08-376-372-2
; Sequence 2, Application US/08376372
; Patent No. 6306840
;  GENERAL INFORMATION:
;    APPLICANT:  Adams, Steven P
;    APPLICANT:  Lin, Ko-Chung
;    APPLICANT:  Lee, Wen-Cherng
;    APPLICANT:  Castro, Alfredo C
;    APPLICANT:  Zimmerman, Craig N
;    APPLICANT:  Hammond, Charles E
;    APPLICANT:  Liao, Yu-Sheng
;    TITLE OF INVENTION:  CELL ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/376,372
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr, James F
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B180
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;      TELEX:  14-8367
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
US-08-376-372-2


  Query Match           100.0%;  Score 23;  DB 4;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          |||||
Db      1 EILDV 5


RESULT  11
PCT-US95-07542-3
; Sequence 3, Application PC/TUS9507542
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  STRUCTURAL MODELS FOR CYTOPLASMIC
;    TITLE OF INVENTION:  DOMAINS OF TRANSMEMBRANE RECEPTORS
;    NUMBER OF SEQUENCES:  20
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/07542
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;      FILING DATE:  13-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/260,514
;      FILING DATE:  15-JUN-1994
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  Ligand sequence recognized by integrin
PCT-US95-07542-3


  Query Match             100.0%;  Score 23;  DB 5;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           |||||
Db       1 EILDV 5


RESULT  12
US-08-271-830-16
; Sequence 16, Application US/08271830
; Patent No. 5510332
;  GENERAL INFORMATION:
;    APPLICANT:  Kogan, Timothy P.
;    APPLICANT:  Ren, Kaijun
;    APPLICANT:  Vanderslice, Peter
;    APPLICANT:  Beck, Pamela J.
;    TITLE OF INVENTION:  A PROCESS OF INHIBITING THE BINDING OF THE
;    TITLE OF INVENTION:  INTEGRIN '4 1 TO VCAM OR FIBRONECTIN AND
;    TITLE OF INVENTION:  LINEAR PEPTIDES THEREFOR
;    NUMBER OF SEQUENCES:  102
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dressler, Goldsmith, Shore & Milnamow, Ltd.
;      STREET:  180 No. 5510332th Stetson, Suite 4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,830
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5510332thrup, Thomas E.
;      REGISTRATION NUMBER:  33,268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312)616-5400
;      TELEFAX:  (312)616-5460
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  /label= Xaa
;      OTHER INFORMATION:  /note= "Xaa=Val-NH2."
US-08-271-830-16


  Query Match             82.6%;  Score 19;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eild 4
           ||||
Db       1 EILD 4


RESULT  13
US-08-860-248C-39
; Sequence 39, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "D CONFIGURATION"
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  2
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "D CONFIGURATION"
US-08-860-248C-39


  Query Match             82.6%;  Score 19;  DB 3;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 eildv 5
           :||||
Db       1 KILDV 5
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RESULT  14
US-09-059-111-8
; Sequence 8, Application US/09059111
; Patent No. 6087330
;  GENERAL INFORMATION:
;    APPLICANT:  Kogan, Timothy P.
;    APPLICANT:  Ren, Kaijun
;    APPLICANT:  Vanderslice, Peter
;    APPLICANT:  Beck, Pamela J.
;    TITLE OF INVENTION:  A Process To Inhibit Binding Of The
;    TITLE OF INVENTION:  Integrin '4  ,To VCAM-1 or Fibronectin And Cyclic Peptides
;    TITLE OF INVENTION:  Therefor
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow, & Katz
;      STREET:  180 No. 6087330th Stetson, 2 Prudential Plaza, Suite
;      STREET:  4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/059,111
;      FILING DATE:  13-APR-1998
;      CLASSIFICATION:  50
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Katz, Martin L.
;      REGISTRATION NUMBER:  25,011
;      REFERENCE/DOCKET NUMBER:  TEX45420132US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  3126165400
;      TELEFAX:  3126165460
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1..5
;      OTHER INFORMATION:  /note= crosslink between Glu at
;      OTHER INFORMATION:  position 1 and Val at position 5.
US-09-059-111-8


  Query Match             82.6%;  Score 19;  DB 3;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          | |||
Db      1 EFLDV 5


RESULT  15
PCT-US95-08353-8
; Sequence 8, Application PC/TUS9508353
;  GENERAL INFORMATION:
;    APPLICANT:  Kogan, Timothy P.
;    APPLICANT:  Ren, Kaijun
;    APPLICANT:  Vanderslice, Peter
;    APPLICANT:  Beck, Pamela J.
;    TITLE OF INVENTION:  A PROCESS TO INHIBIT BINDING OF
;    TITLE OF INVENTION:  THE INTEGRIN '4 1 TO VCAM-1 OR
;    TITLE OF INVENTION:  FIBRONECTIN AND CYCLIC PEPTIDES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dressler, Goldsmith, Shore & Milnamow,
;      ADDRESSEE:  Ltd.
;      STREET:  180 North Stetson, Suite 4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08353
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Northrup, Thomas E.
;      REGISTRATION NUMBER:  33,268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312)616-5400
;      TELEFAX:  (312)616-5460
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1..5
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= crosslink between Glu at position 1 and
;      OTHER INFORMATION:  Val at position 5.
PCT-US95-08353-8


  Query Match             82.6%;  Score 19;  DB 5;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 eildv 5
          | |||
Db      1 EFLDV 5


RESULT  16
US-08-435-286-13
; Sequence 13, Application US/08435286
; Patent No. 5688913
;  GENERAL INFORMATION:
;    APPLICANT:  Arrhenius, Thomas S.
;    APPLICANT:  Elices, Mariano J.
;    APPLICANT:  Gaeta, Federico C.A.
;    TITLE OF INVENTION:  CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dressler, Goldsmith, Shore & Milnamow, Ltd.
;      STREET:  180 No. 5688913th Stetson, Suite 4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,286
;      FILING DATE:
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;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/164,101
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gamson, Edward P.
;      REGISTRATION NUMBER:  29,381
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312)616-5400
;      TELEFAX:  (312)616-5460
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  /label= Xaa
;      OTHER INFORMATION:  /note= "Xaa = Pro-NH2."
US-08-435-286-13


  Query Match             78.3%;  Score 18;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ILDV 4


RESULT  17
US-08-435-286-14
; Sequence 14, Application US/08435286
; Patent No. 5688913
;  GENERAL INFORMATION:
;    APPLICANT:  Arrhenius, Thomas S.
;    APPLICANT:  Elices, Mariano J.
;    APPLICANT:  Gaeta, Federico C.A.
;    TITLE OF INVENTION:  CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS OF USING THE SAME
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dressler, Goldsmith, Shore & Milnamow, Ltd.
;      STREET:  180 No. 5688913th Stetson, Suite 4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,286
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/164,101
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gamson, Edward P.
;      REGISTRATION NUMBER:  29,381
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312)616-5400
;      TELEFAX:  (312)616-5460
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-435-286-14


  Query Match             78.3%;  Score 18;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ILDV 4


RESULT  18
US-08-860-248C-1
; Sequence 1, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  5
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "4-AMINO-BUTYRIC ACID"
US-08-860-248C-1


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ILDV 4


RESULT  19
US-08-860-248C-2
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; Sequence 2, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;   . PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  5
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "4-AMINO-PENTANOIC ACID"
US-08-860-248C-2


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ildv 5
           ||||
Db       1 ILDV 4


RESULT  20
US-08-860-248C-3
; Sequence 3, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  5
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "6-AMINO-HEXANOIC ACID"
US-08-860-248C-3


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ildv 5
           ||||
Db       1 ILDV 4


RESULT  21
US-08-860-248C-4
; Sequence 4, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  4:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  5
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "7-AMINO-HEPTANOIC ACID"
US-08-860-248C-4


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ILDV 4


RESULT  22
US-08-860-248C-5
; Sequence 5, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  5
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "7-AMINO-HEXANOIC ACID"
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "D CONFIGURATION"
US-08-860-248C-5


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      1 ILDV 4


RESULT  23
US-08-860-248C-11
; Sequence 11, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-D-LYSINE"
US-08-860-248C-11


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      2 ILDV 5


RESULT  24
US-08-860-248C-12
; Sequence 12, Application US/08860248C
; Patent No. 6034056
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;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-D-ORNITHINE"
US-08-860-248C-12


  Query Match           78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ildv 5
           ||||
Db       2 ILDV 5


RESULT  25
US-08-860-248C-13
; Sequence 13, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-ORNITHINE"
US-08-860-248C-13


  Query Match           78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ildv 5
           ||||
Db       2 ILDV 5


RESULT  26
US-08-860-248C-14
; Sequence 14, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
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;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-D-LYSINE"
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  2
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "D CONFIGURATION"
US-08-860-248C-14


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ildv 5
           ||||
Db       2 ILDV 5


RESULT  27
US-08-860-248C-15
; Sequence 15, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  5
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "4-AMINOMETHYL-BENZOIC ACID"
US-08-860-248C-15


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ildv 5
           ||||
Db       1 ILDV 4


RESULT  28
US-08-860-248C-16
; Sequence 16, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  5
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "(4-(2-AMINOETHYL)-IMIDAZOL-1-YL)-
;      OTHER INFORMATION:  ACETIC ACID"
US-08-860-248C-16


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ildv 5
           ||||
Db       1 ILDV 4


RESULT  29
US-08-860-248C-20
; Sequence 20, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
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;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-D-LYSINE"
US-08-860-248C-20


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      2 ILDV 5


RESULT  30
US-08-860-248C-21
; Sequence 21, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-ORNITHINE"
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  2
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "D-CONFIGURATION"
US-08-860-248C-21


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      2 ILDV 5


RESULT  31
US-08-860-248C-22
; Sequence 22, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
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;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-D-ORNITHINE"
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  2
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "D-CONFIGURATION"
US-08-860-248C-22


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ildv 5
          ||||
Db      2 ILDV 5


RESULT  32
US-08-860-248C-23
; Sequence 23, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-LYSINE"
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  2
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "D-CONFIGURATION"
US-08-860-248C-23


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
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Qy      2 ildv 5
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Db      2 ILDV 5


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US-08-860-248C-24
; Sequence 24, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-2,4-DIAMINO-BUTYRIC ACID"
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  2
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "D-CONFIGURATION"
US-08-860-248C-24


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
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Db       2 ILDV 5


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; Sequence 25, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
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;      NAME/KEY:  Peptide
;      LOCATION:  1
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US-08-860-248C-25


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
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Qy       2 ildv 5
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Db       2 ILDV 5


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; Sequence 26, Application US/08860248C
; Patent No. 6034056
;  GENERAL INFORMATION:
;    APPLICANT:  DUTTA, Anand
;    TITLE OF INVENTION:  FIBRONECTIN ADHESION INHIBITORS
;    NUMBER OF SEQUENCES:  122
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pillsbury Madison & Sutro, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MS WORD
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,248C
;      FILING DATE:  24-JUNE-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426254.0
;      FILING DATE:  24-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9505905.1
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513904.4
;      FILING DATE:  07-JUL-1995
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1
;      OTHER INFORMATION:  /product= "OTHER"
;      OTHER INFORMATION:  /note= "N-ACETYL-2,4-DIAMINO-BUTYRIC ACID, D
;      OTHER INFORMATION:  CONFIGURATION"
US-08-860-248C-26


  Query Match             78.3%;  Score 18;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ildv 5
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Db       2 ILDV 5


Search completed: June 10, 2002, 06:37:15
Job time: 38 sec
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L2          512 S EILDV/SQSP
L3          496 S L2 NOT L1
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               SAV L3 GAM251073B/A

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     FILE 'HCAPLUS' ENTERED AT 08:02:59 ON 10 JUN 2002
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L6          351 S L3
L7            9 S EILDV
               E LOBB R/AU
L8          113 S E3,E5,E7,E8
               E BURKLY L/AU
L9           82 S E3-E6
               E BIOGEN/PA,CS
L10         647 S E3-E56
L11           4 S L5-L7 AND L8-L10
L12         363 S L5-L7
L13           2 S L12 AND ?ASTHMA?
               E ASTHMA/CT
               E E3+ALL
L14        9231 S E2+NT
               E E4+ALL
L15        6156 S E6,E5+NT
               E E10+ALL
               E E5+ALL
L16        8875 S E5,E4+NT
               E E11+ALL
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L17         681 S E4,E3+NT
L18           1 S L12 AND L14-L17
L19          35 S L12 AND (LUNG OR PULMON? OR AIRWAY OR AIR WAY OR BRONCH? OR R
L20           2 S L13,L18
               E RESPIR/CT
               E E13+ALL
L21       38379 S E5,E4+NT
L22         944 S E36+NT
               E E38+ALL
L23      115430 S E4+NT
               E E3+AKK
               E E3+ALL
               E E73+ALL
L24         700 S E2
               E RESPIRATORY TRACT/CT
               E E42+ALL
L25         177 S E1
               E E2+ALL
L26      115430 S E4+NT
L27          18 S L12 AND L21-L26
L28          18 S L27 AND L19
L29          23 S L20,L28,L11
L30          16 S L19 NOT L29
L31           1 S L30 AND RESPIRATORY DISTRESS SYNDROME
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Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

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L32          24 S L29,L31
L33           3 S L12 AND HYPERSENSITIV?
L34           3 S L12 AND ?ALLERG?
L35           5 S L33,L34
L36           1 S L35 AND L32
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L40           1 S L39 AND L13,L18
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L44           4 S L11,L20 NOT L43
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=> fil hcaplus
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FILE COVERS 1907 - 10 Jun 2002  VOL 136 ISS 24
FILE LAST UPDATED: 7 Jun 2002  (20020607/ED)

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 substance identification.

CAS roles have been modified effective December 16, 2001. Please
check your SDI profiles to see if they need to be revised. For
information on CAS roles, enter HELP ROLES at an arrow prompt or use
the CAS Roles thesaurus (/RL field) in this file.

=> d 143 all tot

L43  ANSWER 1 OF 2  HCAPLUS  COPYRIGHT 2002 ACS
AN   1999:505686  HCAPLUS
DN   131:139496
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TI Fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions
IN Arrhenius, Thomas S.; Elices, Mariano J.; Gaeta, Federico C. A.
PA Cytel Corporation, USA
SO U.S., 81 pp.
CODEN: USXXAM
DT Patent
LA English
IC ICM C07K005-08
NCL 530331000
CC 1-7 (Pharmacology)
Section cross-reference(s): 34, 63
FAN.CNT 4

	PATENT NO.	KIND	DATE		APPLICATION NO.	DATE	
PI	US 5936065	A	19990810		US 1995-462424	19950605	<--
	CA 2177840	AA	19950615		CA 1994-2177840	19941205	<--
	CN 1142832	A	19970212		CN 1994-194969	19941205	<--
	US 5688913	A	19971118		US 1995-435286	19950505	<--
	US 6117840	A	20000912		US 1997-837154	19970414	<--
	US 6103870	A	20000815		US 1997-923026	19970903	<--
PRAI	US 1993-164101	B2	19931206	<--			
	US 1994-349024	B2	19941202				
	US 1995-435286	A1	19950505				

OS MARPAT 131:139496
AB Peptidomimetic compds. are disclosed that inhibit the binding between the VLA-4 and the fibronectin CS-1 compd. Pharmaceutical compns. contg. a contemplated compd. and methods for treating immunoinflammatory conditions using the compd. are also disclosed.
ST fibronectin CS1 VLA4 binding inhibitor peptidomimetic; immunoinflammatory disease pharmaceutical peptidomimetic; inflammation inhibitor peptidomimetic
IT Cell adhesion molecules
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(ICAM-1 (intercellular adhesion mol. 1); fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)
IT Animal cell line
(JURKAT; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)
IT Histocompatibility antigens
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(MHC (major histocompatibility complex), class II; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)
IT Cell adhesion molecules
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(VCAM-1; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)
IT Transplant and Transplantation
Transplant and Transplantation
(allotransplant, heart; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)
IT Heart
(allotransplant; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)
IT Encephalomyelitis
(autoimmune; fibronectin CS-1 peptidomimetics for inhibiting binding of

CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Artery
(coronary; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT **Allergy**
(delayed **hypersensitivity**; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Immunity
(disorder; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Anti-inflammatory agents
Antiasthmatics
Antirheumatic agents
Immunosuppressants
Macrophage
Peptidomimetics
Rheumatoid arthritis
Structure-activity relationship
T cell (lymphocyte)
(fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Fibronectins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Cell migration
(lymphocyte; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Drug delivery systems
(prodrugs; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Multiple sclerosis
(therapeutic agents; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT Integrins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(.alpha.4.beta.1; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT 125850-12-6 **126235-03-8 150525-67-0** 153982-81-1
184293-88-7 236100-96-2 236100-98-4 **236100-99-5**
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236101-03-4 **236101-04-5 236101-05-6** 236101-06-7
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT 7440-53-1D, Europium, complexes with peptidomimetics, biological studies
38763-90-5 77292-72-9 164740-10-7 177081-20-8 177081-48-0
177081-49-1 184293-89-8 184293-90-1 184293-91-2 184293-92-3
209600-74-8 209600-76-0 209600-77-1 209600-78-2 209600-79-3
209600-80-6 209600-82-8 209600-83-9 209600-84-0 209600-85-1
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209602-74-4 209602-75-5 209602-76-6 209602-77-7 209602-78-8
209602-79-9 209602-80-2 209602-81-3 209602-82-4 236100-75-7
236100-89-3 236100-91-7 236100-94-0
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT 17186-57-1P 120125-44-2P 170986-07-9P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(prepn. and reaction; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

IT 103-82-2, Phenylacetic acid, reactions 110-91-8, Morpholine, reactions 7536-58-5 13139-15-6 13734-34-4
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction; fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Anon; EP 361977 1990 HCAPLUS
(2) Anon; WO 91/03252 1991 HCAPLUS
(3) Anon; WO 93/12809 1993 HCAPLUS
(4) Eliccs, M; Cell Adhesion and Human Disease, Ciba Foundation Symposium 189 1995, P79
(5) Furcht; US 5294511 1994 HCAPLUS
(6) Ioria; J Med Chem 1991, V34, P2615
(7) Komoriya, A; J Biol Chem 1991, V266, P15075 HCAPLUS
(8) Mousa, S; Clin Pharm 1993, V83, P373
(9) Mumford; US 5387504 1995 HCAPLUS
(10) Nowlin, D; J Biol Chem 1993, V268, P20352 HCAPLUS
(11) Pfaff, M; J Biol Chem 1994, V269, P20233 HCAPLUS
(12) Snyderman; US 4822606 1989 HCAPLUS

L43 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2002 ACS
AN 1997:207658 HCAPLUS

DN **126:199840**
TI Preparation of peptide derivatives as cell adhesion inhibitors
IN Lin, Ko-Chung; Adams, Steven P.; Castro, Alfredo C.; Zimmerman, Craig N.; Cuervo, Julio Hernan; Lee, Wen-Cherng; Hammond, Charles E.; Carter, Mary Beth; Almquist, Ronald G.; Ensinger, Carol Lee
PA **Biogen, Inc., USA**; Lin, Ko-Chung; Adams, Steven, P.; Castro, Alfredo, C.; Zimmerman, Craig, N.; Cuervo, Julio, Hernan; Lee, Wen-Cherng; Hammond, Charles, E.; Carter, Mary, Beth; et al.
SO PCT Int. Appl., 117 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C07K014-78
ICS C07K005-02; C07K005-06; C07K005-08; C07K005-10; A61K038-04; A61K038-39
CC 34-3 (Amino Acids, Peptides, and Proteins)
Section cross-reference(s): 1, 63
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9703094	A1	19970130	WO 1996-US11570	19960711
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	US 6248713	B1	20010619	US 1995-498237	19950711
	CA 2226868	AA	19970130	CA 1996-2226868	19960711
	AU 9664894	A1	19970210	AU 1996-64894	19960711
	AU 716276	B2	20000224		
	EP 842196	A1	19980520	EP 1996-924444	19960711
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI				
	CN 1193325	A	19980916	CN 1996-196380	19960711
	BR 9609782	A	19990309	BR 1996-9782	19960711
	JP 11511124	T2	19990928	JP 1996-505989	19960711
	FI 9800033	A	19980305	FI 1998-33	19980109
	NO 9800097	A	19980311	NO 1998-97	19980109
	US 6239108	B1	20010529	US 1998-983391	19980810
PRAI	US 1995-498237	A	19950711		
	WO 1996-US11570	W	19960711		

OS MARPAT 126:199840
AB The present invention relates to novel peptide derivs. that are useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compds. and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compds. and pharmaceutical compn. of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases. Thus, coupling of 4-(2-MeC6H4NHCONH)C6H4CH2CO2H (prepn. given) with protected peptide H-Leu-Asp(OCH2Ph)-Val-OCH2Ph (prepn. given), followed by catalytic hydrogenolysis, gave cell adhesion inhibitor peptide 4-(2-MeC6H4NHCONH)C6H4CH2CO-Leu-Asp-Val-OH (I). All 408 prepd. peptide derivs., including I, inhibited VLA4-dependent adhesion to a bovine serum albumin conjugate with H-Cys-Tyr-Asp-Glu-Leu-Pro-Gln-Leu-Val-Thr-Leu-Pro-His-Pro-Asn-Leu-His-Gly-Pro-Glu-Ile-Leu-Asp-Val-Pro-Ser-Thr-OH, with IC50 values of <1 mM.
ST peptide prepn cell adhesion inhibitor; antiinflammatory drug peptide deriv prepn; autoimmune disease treatment peptide deriv prepn
IT Cell adhesion
(inhibitors; prepn. of peptide derivs. as cell adhesion inhibitors)

IT Anti-inflammatory drugs
Autoimmune diseases
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT Peptides, preparation
RL: BAC (Biological activity or effector, except adverse); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 187737-58-2P
RL: BAC (Biological activity or effector, except adverse); RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of peptide derivs. as cell adhesion inhibitors)

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187736-21-6P 187736-22-7P 187736-23-8P 187736-24-9P 187736-25-0P
RL: BAC (Biological activity or effector, except adverse); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(prepn. of peptide derivs. as cell adhesion inhibitors)

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187738-08-5P 187834-08-8P
RL: BAC (Biological activity or effector, except adverse); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT **187738-30-3DP**, conjugate with bovine serum albumin
RL: BPR (Biological process); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 74-89-5, Methylamine, reactions 75-31-0, Isopropylamine, reactions 78-81-9, Isobutylamine 93-10-7, 2-Quinolinecarboxylic acid 95-55-6, 2-Hydroxyaniline 98-09-9, Phenylsulfonyl chloride 98-68-0, 4-Methoxybenzenesulfonyl chloride 98-98-6, Picolinic acid 100-46-9, Benzylamine, reactions 103-71-9, Phenyl isocyanate, reactions 103-80-0, Phenylacetyl chloride 108-91-8, Cyclohexylamine, reactions 110-89-4, Piperidine, reactions 110-91-8, Morpholine, reactions 348-54-9, 2-Fluoroaniline 501-52-0, Hydrocinnamic acid 501-97-3, 3-(4-Hydroxyphenyl)propionic acid 504-29-0, 2-Aminopyridine 614-68-6, o-Tolyl isocyanate 1197-55-3, 4-Aminophenylacetic acid 1603-40-3, 2-Amino-3-methylpyridine 2393-23-9, 4-Methoxybenzylamine 2462-31-9, Glycine benzyl ester hydrochloride 2577-48-2, Proline methyl ester 2620-50-0, Piperonylamine 2748-02-9 3373-59-9, Threonine methyl ester 3392-09-4 3392-12-9 3845-64-5 4070-48-8, Valine methyl ester 5081-36-7, 3-Methoxy-4-nitrobenzoic acid 6066-82-6, N-Hydroxysuccinimide 6624-49-3, 3-Isoquinolinecarboxylic acid 7531-52-4 7536-58-5 13139-15-6 13734-41-3 13798-75-9 15761-39-4 16013-85-7, 2,6-Dichloro-3-nitropyridine 16369-05-4, Valinol 18496-54-3, 4-Phenylbutyryl chloride 21760-98-5, Valine benzyl ester 33797-51-2,

Eschenmoser's salt 38068-75-6 39552-81-3, Methyl p-aminophenylacetate
41324-66-7, Proline benzyl ester 42726-73-8, tert-Butyl methyl malonate
53308-95-5 53363-89-6 129460-09-9 135892-76-1
RL: RCT (Reactant)
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 5803-22-5P 40851-91-0P 67579-92-4P, 3-Methoxy-4-nitrobenzoyl chloride
90323-26-5P 136465-99-1P 153982-81-1P 181517-99-7P 181518-01-4P
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187738-34-7P 187738-35-8P 187738-36-9P 187738-37-0P 187738-38-1P
187738-39-2P 187738-40-5P 187738-41-6P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation)
(prepn. of peptide derivs. as cell adhesion inhibitors)

IT 38533-61-8P
RL: SPN (Synthetic preparation); PREP (Preparation)
(prepn. of peptide derivs. as cell adhesion inhibitors)

=> fil reg
FILE 'REGISTRY' ENTERED AT 08:26:18 ON 10 JUN 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

STRUCTURE FILE UPDATES: 7 JUN 2002 HIGHEST RN 427375-75-5
DICTIONARY FILE UPDATES: 7 JUN 2002 HIGHEST RN 427375-75-5

TSCA INFORMATION NOW CURRENT THROUGH January 7, 2002

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES
for more information. See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=> d sqide can tot l46

L46 ANSWER 1 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **236101-05-6** REGISTRY
CN L-Proline, L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 6

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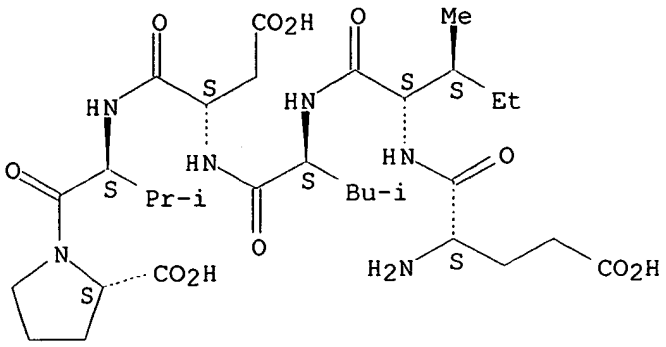
MF C31 H52 N6 O11
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.



1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 131:139496

L46 ANSWER 2 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **236101-04-5** REGISTRY
CN L-Valine, L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 6

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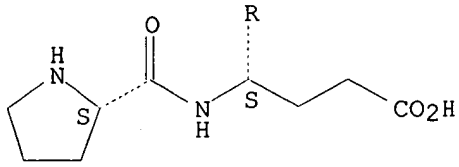
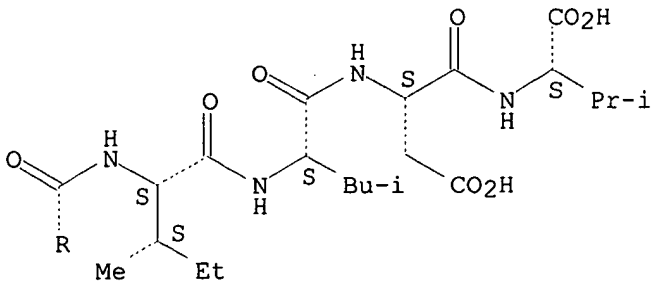
MF C31 H52 N6 O11
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.





1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 131:139496

L46 ANSWER 3 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **236101-02-3** REGISTRY
CN L-Valine, L-leucyl-L-histidylglycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
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SEQ 1 LHGPEILDV
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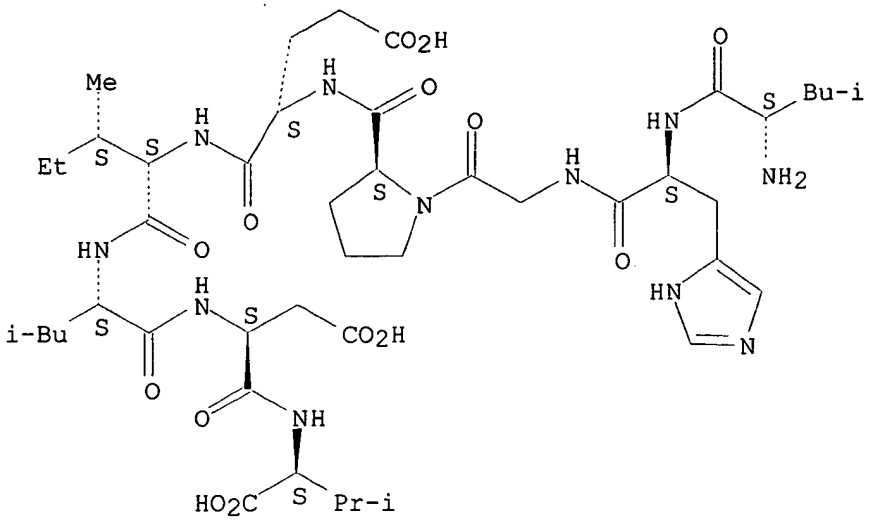
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.



1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 131:139496

L46 ANSWER 4 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **236101-01-2** REGISTRY
CN L-Proline, L-histidylglycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
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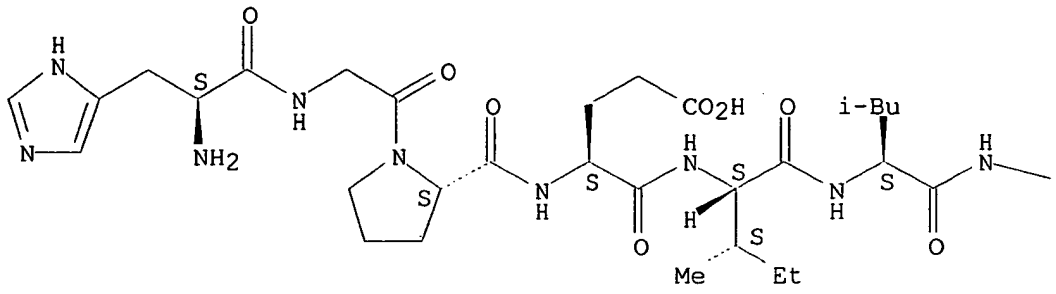
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A



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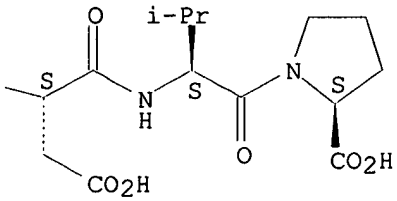

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REFERENCE 1: 131:139496

L46 ANSWER 5 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **236101-00-1** REGISTRY
CN L-Serine, glycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 9

SEQ 1 GPEILDVPS
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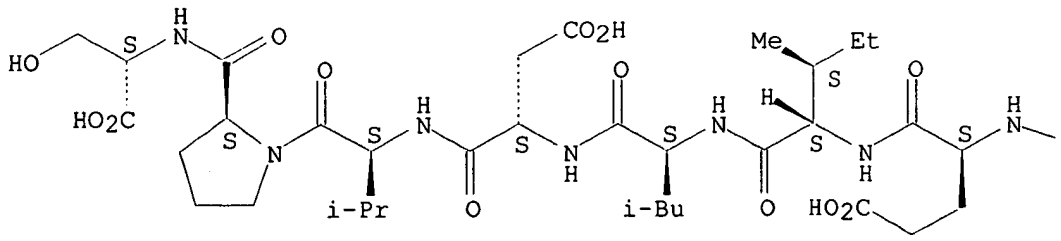
MF C41 H67 N9 O15
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A



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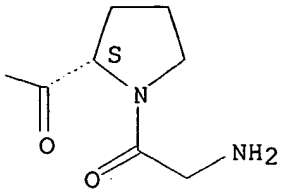

1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 131:139496

L46 ANSWER 6 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **236100-99-5** REGISTRY
CN L-Valine, L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl-L-threonyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 9

SEQ 1 EILDVPSTV
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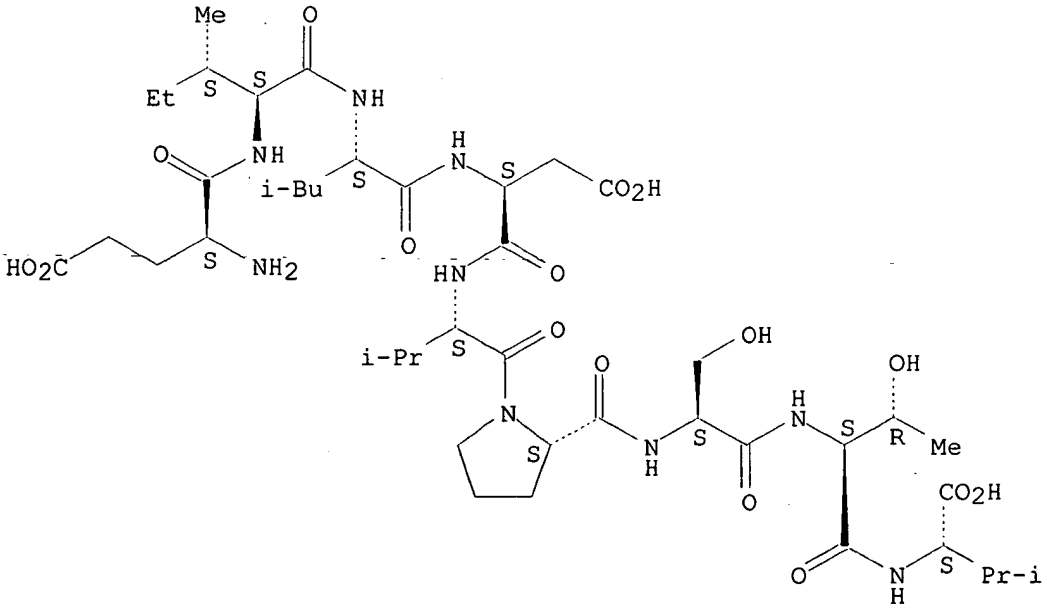
HITS AT: 1-5
MF C43 H73 N9 O16
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.



1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 131:139496

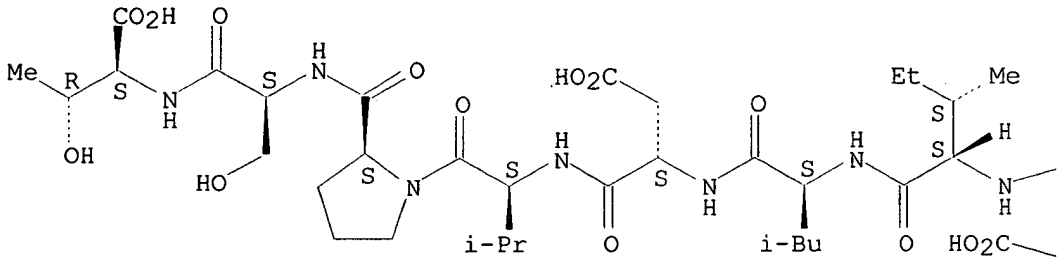
L46 ANSWER 7 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **187738-30-3** REGISTRY
CN L-Threonine, L-cysteinyl-L-tyrosyl-L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-leucyl-L-prolyl-L-glutaminyl-L-leucyl-L-valyl-L-threonyl-L-leucyl-L-prolyl-L-histidyl-L-prolyl-L-asparaginyl-L-leucyl-L-histidylglycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4: PN: US6376538 SEQID: 4 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 27

SEQ 1 CYDELPQLVT LPHPNLHGPE ILDVPST
= ====

HITS AT: 20-24
MF C135 H209 N33 O42 S
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A



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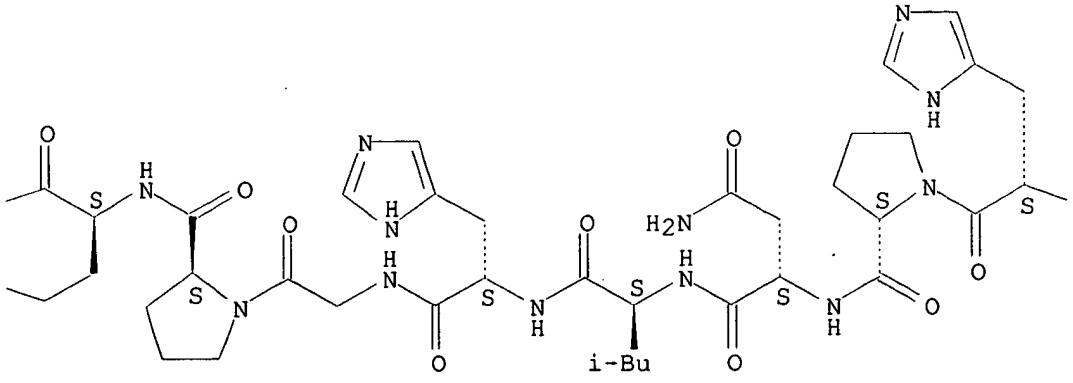

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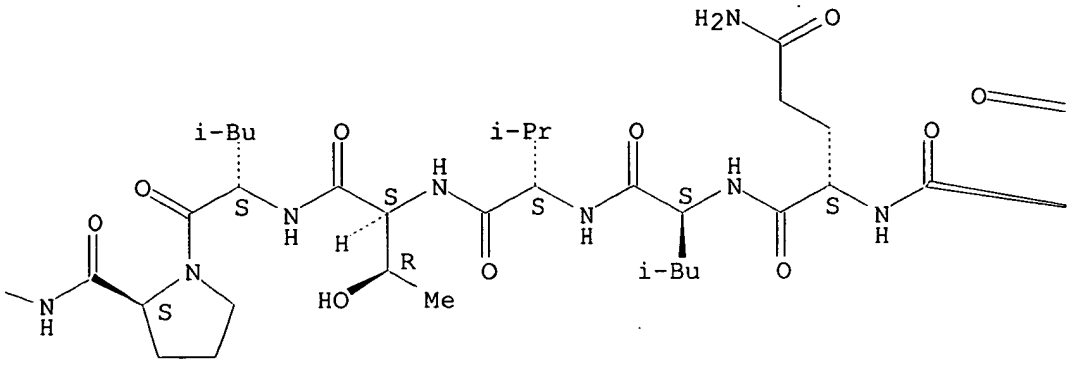

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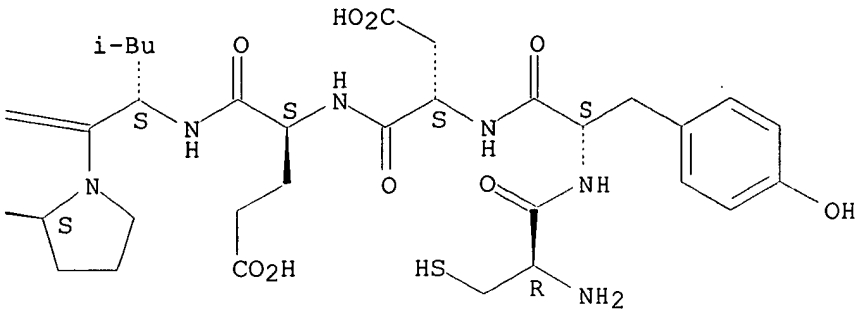

2 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
2 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 136:325828

REFERENCE 2: 126:199840

L46 ANSWER 8 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **150525-67-0** REGISTRY
CN L-Valine, L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN L-Valine, N-[N-[N-(N-L-.alpha.-glutamyl-L-isoleucyl)-L-leucyl]-L-.alpha.-aspartyl]-
OTHER NAMES:
CN 23: PN: WO0004941 PAGE: 32 claimed sequence
CN 2: PN: US6376538 SEQID: 2 unclaimed sequence
CN 2: PN: WO0064474 PAGE: 19 unclaimed sequence
CN 457: PN: WO0069900 SEQID: 1142 unclaimed sequence
CN PN: US5962311 SEQID: 2 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL **5**

SEQ 1 EILDV
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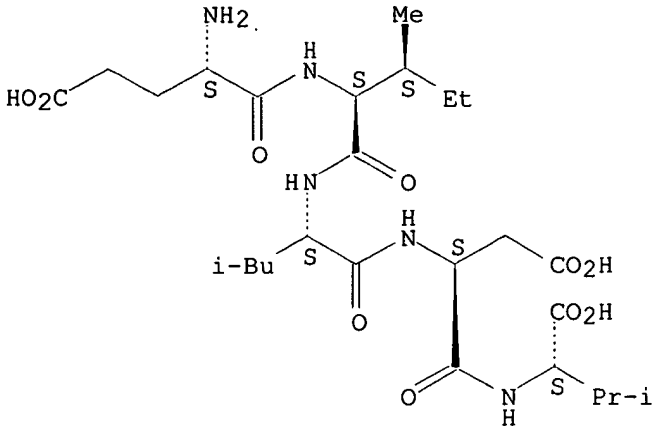
HITS AT: 1-5

MF C26 H45 N5 O10
SR CA
LC STN Files: CA, CAPLUS, CHEMCATS, TOXCENTER, USPATFULL

Absolute stereochemistry.



16 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
16 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 136:325828

REFERENCE 2: 135:368937

REFERENCE 3: 134:21425

REFERENCE 4: 133:334056

REFERENCE 5: 132:142003

REFERENCE 6: 131:267956

REFERENCE 7: 131:139496

REFERENCE 8: 128:150383

REFERENCE 9: 128:18371

REFERENCE 10: 126:176918

L46 ANSWER 9 OF 9 REGISTRY COPYRIGHT 2002 ACS
RN **126235-03-8** REGISTRY
CN L-Threonine, glycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl- (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN L-Threonine, N-[N-[1-[N-[N-[N-[N-[N-(1-glycyl-L-prolyl)-L-.alpha.-glutamyl]-L-isoleucyl]-L-leucyl]-L-.alpha.-aspartyl]-L-valyl]-L-prolyl]-L-seryl]-
OTHER NAMES:
CN 24: PN: WO0192542 SEQID: 25 claimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 10

SEQ 1 GPEILDVPST

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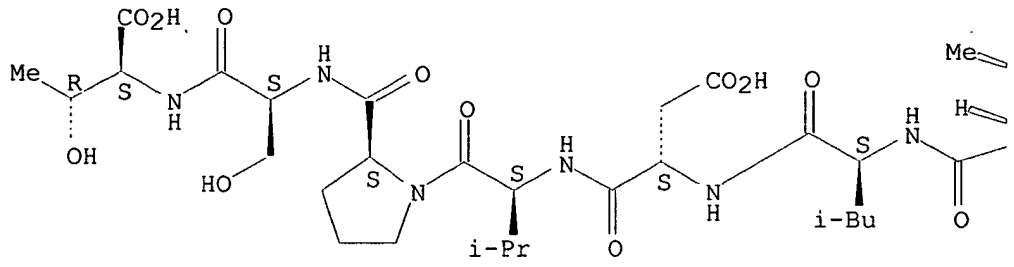
HITS AT: 3-7
MF C45 H74 N10 O17
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A



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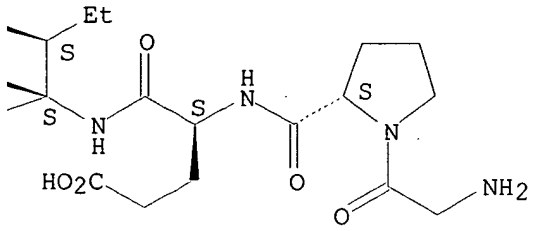

11 REFERENCES IN FILE CA (1967 TO DATE)
11 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 136:32634

REFERENCE 2: 131:139496

REFERENCE 3: 130:163180

REFERENCE 4: 129:245488

REFERENCE 5: 126:14475

REFERENCE 6: 120:215235

REFERENCE 7: 119:201761

REFERENCE 8: 115:270674

REFERENCE 9: 115:254061

REFERENCE 10: 115:229941

=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 08:26:38 ON 10 JUN 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE COVERS 1907 - 10 Jun 2002 VOL 136 ISS 24
FILE LAST UPDATED: 7 Jun 2002 (20020607/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

=> d all tot 144

L44 ANSWER 1 OF 4 HCAPLUS COPYRIGHT 2002 ACS
AN 2002:312019 HCAPLUS
DN 136:325828
TI Preparation of dipeptide derivatives as cell adhesion inhibitors
IN Adams, Steven P.; Lin, Ko-Chung; Lee, Wen-Cherng; Castro, Alfredo C.; Zimmerman, Craig N.; Hammond, Charles E.; Liao, Yu-Sheng; Cuervo, Julio Hernan; Singh, Juswinder
PA **Biogen, Inc., USA**
SO U.S., 50 pp., Cont.-in-part of U.S. 6,306,840.
CODEN: USXXAM
DT Patent
LA English
IC ICM A61K031-357
ICS C07D317-46
NCL 514466000
CC 34-3 (Amino Acids, Peptides, and Proteins)
Section cross-reference(s): 1
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6376538	B1	20020423	US 1997-875321	19970919
	US 6306840	B1	20011023	US 1995-376372	19950123
	WO 9622966	A1	19960801	WO 1996-US1349	19960118
	W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE				
	EP 1142867	A2	20011010	EP 2001-107877	19960118
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI				
PRAI	US 1995-376372	A2	19950123		
	WO 1996-US1349	W	19960118		
	EP 1996-905316	A3	19960118		

OS MARPAT 136:325828
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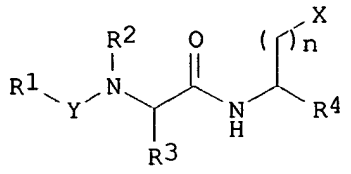

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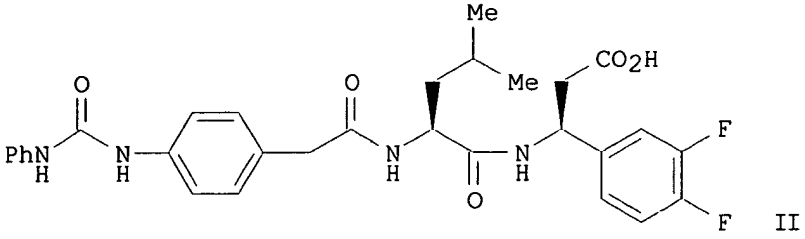

II

AB Novel dipeptide analogs I [X = CO2H, PO3H-, SO2R5, SO3H, OPO3H-, CO2R4; Y = CO, SO2, PO2; n = 0-2; R1 = optionally substituted alkyl, alkenyl, alkynyl, aryl-fused cycloalkyl, cycloalkenyl, aryl, aralkyl, aralkenyl, aralkynyl, alkoxy, alkenyloxy, aralkoxy, alkylamino, alkenylamino, alkynylamino, aryloxy, arylamino, N-alkylurea-substituted alkyl, heterocyclyl; R2 = H, aryl, alkyl, alkenyl, alkynyl, cycloalkyl, cycloalkenyl, aralkyl; R2NCR3 = heterocyclic ring; R3 = natural, unnatural, modified, or substituted amino acid side chain; R4 = optionally substituted aryl, alkyl, cycloalkyl, alkenyl, cycloalkenyl, alkynyl, aralkyl, H, heterocyclyl, heterocyclylcarbonyl, aminocarbonyl, amido, alkylaminocarbonyl, arylaminocarbonyl, acylaminocarbonyl, acyl; R5 = alkyl, alkenyl, alkynyl, cycloalkyl, cycloalkenyl, aryl, aralkyl, aralkenyl, aralkynyl] are prepd. as compds. useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compds. and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compds. and pharmaceutical compns. of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases. Thus, .beta.-amino acid-contg. dipeptide II, prepd. by std. methods, displayed an IC50 of <50 nM in a cell adhesion inhibition assay.

ST cell adhesion inhibitor dipeptide analog prepn; aminoacyl amino acid prepn antiinflammatory

IT Anti-inflammatory agents
Cell adhesion
(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT Dipeptides
RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 181518-22-9P 181521-43-7P
RL: PAC (Pharmacological activity); RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion

inhibitors)

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181523-52-4P 181523-55-7P 181523-57-9P 181523-60-4P 181523-61-5P

RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 181523-62-6P 181523-63-7P 181523-65-9P 181523-67-1P 181523-68-2P
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181523-77-3P 181523-78-4P 181525-84-8P 181525-85-9P 181525-86-0P
181525-87-1P 181526-54-5P 181783-03-9P 181783-04-0P

RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 52-90-4, L-Cysteine, reactions 60-32-2, 6-Aminohexanoic acid 65-45-2,

Salicylamide 75-36-5, Acetyl chloride 96-50-4, 2-Aminothiazole 98-09-9, Phenylsulfonyl chloride 100-28-7, 4-Nitrophenyl isocyanate 103-71-9, Phenyl isocyanate, reactions 103-82-2, Phenylacetic acid, reactions 104-03-0, 4-Nitrophenylacetic acid 117-34-0, Diphenylacetic acid 122-78-1, Phenylacetaldehyde 123-90-0, Thiomorpholine 124-40-3, Dimethylamine, reactions 124-63-0, Methanesulfonyl chloride 140-10-3, (E)-Cinnamic acid, reactions 141-82-2, Malonic acid, reactions 150-13-0, 4-Aminobenzoic acid 156-38-7, 4-Hydroxyphenylacetic acid 372-09-8, Cyanoacetic acid 459-57-4, 4-Fluorobenzaldehyde 500-22-1, 3-Pyridinecarboxaldehyde 504-29-0, 2-Aminopyridine 581-96-4, 2-Naphthylacetic acid 614-68-6, 2-Methylphenyl isocyanate 621-29-4, 3-Methylphenyl isocyanate 624-83-9, Methyl isocyanate 643-28-7, 2-Isopropylaniline 700-87-8, 2-Methoxyphenyl isocyanate 768-56-9, 4-Phenyl-1-butene 771-50-6, Indole-3-carboxylic acid 943-89-5 1011-54-7 1121-60-4, 2-Pyridinecarboxaldehyde 1189-71-5, Chlorosulfonyl isocyanate 1197-55-3, 4-Aminophenylacetic acid 1571-08-0, Methyl 4-formylbenzoate 3173-53-3, Cyclohexyl isocyanate 3320-86-3, 2-Nitrophenyl isocyanate 3392-09-4 3392-10-7 3397-35-1 3886-69-9, (R)-.alpha.-Methylbenzylamine 5068-28-0 5081-36-7, 3-Methoxy-4-nitrobenzoic acid 5292-21-7, Cyclohexylacetic acid 5678-48-8 5856-77-9, 2,2-Dimethylbutyryl chloride 6120-95-2, 1-Phenyl-1-cyclopropanecarboxylic acid 6335-76-8 14338-36-4, 3-Aminophenylacetic acid 14381-41-0 14381-42-1, 1-Indanecarboxylic acid 14737-89-4, (E)-3,4-Dimethoxycinnamic acid 14898-52-3, Benzenepropanoic acid, .beta.-amino-, Methyl ester 15100-75-1, Phenylalanine tert-butyl ester hydrochloride 16013-85-7, 2,6-Dichloro-3-nitropyridine 16947-80-1 17570-26-2, (E)-3-Methoxycinnamic acid 17859-70-0 18496-54-3, 4-Phenylbutyryl chloride 18598-74-8, Isoleucine methyl ester hydrochloride 19686-73-8, 1-Bromo-2-propanol 19947-39-8 26348-68-5 29668-44-8 30925-18-9 34036-07-2, 3,4-Difluorobenzaldehyde 34404-36-9 35000-38-5, tert-Butoxycarbonylmethylenetriphenylphosphorane 35161-71-8, N-Methylpropargylamine 38489-76-8, (E)-3,4-Methylenedioxycinnamic acid 39552-81-3, Methyl p-aminophenylacetate 39931-77-6, Ethyl 3-pyridylacetate 42726-73-8, tert-Butyl methyl malonate 60280-45-7 67579-92-4, 3-Methoxy-4-nitrobenzoyl chloride 71510-77-5 88950-64-5, 1-(tert-Butoxycarbonylamino)cyclopropanecarboxylic acid 128593-66-8 136465-99-1 149193-92-0 174579-31-8 181517-97-5 181517-98-6 181517-99-7 181518-00-3 181518-01-4 181518-02-5
RL: RCT (Reactant); RACT (Reactant or reagent)
(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 325-89-3P 3423-47-0P 3901-07-3P 5467-09-4P 6404-29-1P 7042-36-6P, tert-Butyl (E)-cinnamate 30461-77-9P, Methyl (E)-3,4-dimethoxycinnamate 30914-88-6P 38533-61-8P 38693-90-2P 39658-45-2P 40851-91-0P 40918-96-5P, Methyl (E)-3,4-methylenedioxycinnamate 40918-98-7P 53484-52-9P 56309-56-9P 70232-19-8P 70232-20-1P 73158-83-5P 74405-07-5P 90323-26-5P 98288-15-4P 100891-10-9P 120686-18-2P 124082-19-5P 129042-97-3P 154457-63-3P 158849-23-1P 159848-76-7P 166023-31-0P 174891-02-2P 181517-73-7P 181517-74-8P 181517-75-9P 181517-76-0P 181517-77-1P 181517-78-2P 181517-80-6P 181517-82-8P 181517-83-9P 181517-85-1P 181517-86-2P 181517-87-3P 181517-88-4P 181517-89-5P 181517-90-8P 181517-91-9P 181517-92-0P 181517-93-1P 181517-94-2P 181517-95-3P 181517-96-4P 181518-04-7P 181518-05-8P 181518-06-9P 181518-07-0P 181518-08-1P 181518-09-2P 181518-10-5P 181518-11-6P 181518-12-7P 181518-14-9P 181518-15-0P 181518-17-2P 181518-19-4P 181518-20-7P 181518-24-1P 181518-25-2P 181518-27-4P 181518-28-5P 181518-30-9P 181518-32-1P 181518-34-3P 181518-36-5P 181518-37-6P 181518-38-7P 181518-39-8P 181518-40-1P 181518-41-2P 181518-42-3P 181518-43-4P 181518-44-5P 181518-46-7P 181518-47-8P 181518-48-9P 181518-49-0P 181518-50-3P 181518-51-4P 181518-52-5P 181518-53-6P 181518-54-7P 181518-55-8P 181518-56-9P 181518-57-0P 181518-58-1P 181518-59-2P

181518-60-5P 181518-61-6P 181518-62-7P 181518-63-8P 181518-64-9P
181518-65-0P 181518-66-1P 181518-67-2P 181518-68-3P 181518-69-4P
181518-70-7P 181518-71-8P 181518-72-9P 181518-73-0P 181518-74-1P
181518-76-3P 181518-77-4P 181518-78-5P 181518-79-6P 181518-80-9P
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181518-88-7P 181518-89-8P 181518-90-1P 181518-91-2P 181518-92-3P
181518-93-4P 181518-94-5P 181518-95-6P 181518-96-7P 181518-97-8P
181518-98-9P 181518-99-0P 181519-00-6P 181519-01-7P 181519-02-8P
181519-03-9P 181519-05-1P 181519-06-2P 181519-07-3P 181519-08-4P
181519-09-5P 181519-10-8P 181519-11-9P 181519-12-0P 181519-13-1P
181519-15-3P 181519-16-4P 181519-17-5P 181519-18-6P 181519-19-7P
181519-20-0P 181519-21-1P 181519-22-2P 181519-23-3P 181519-25-5P
181519-26-6P 181519-27-7P 181519-28-8P 181519-29-9P 181519-30-2P
181519-31-3P 181519-32-4P 181519-33-5P 181519-34-6P 181519-35-7P
181519-36-8P 181519-37-9P 181519-38-0P 181519-39-1P 181519-40-4P
181519-41-5P 181519-42-6P 181519-43-7P 181519-44-8P 181519-45-9P
181519-46-0P 181519-47-1P 181519-48-2P 181519-49-3P 181519-50-6P
181519-51-7P 181519-52-8P 181519-54-0P 181519-55-1P 181519-56-2P
181519-57-3P 181519-58-4P 181519-59-5P 181519-60-8P 181519-61-9P
181519-62-0P 181519-63-1P 181519-64-2P 181519-65-3P 181519-66-4P
181519-67-5P 181519-68-6P 181519-69-7P 181519-70-0P 181519-71-1P
181519-72-2P 181519-73-3P 181519-75-5P 181519-76-6P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT 181519-89-1P
RL: SPN (Synthetic preparation); PREP (Preparation)
(prepn. of .beta.-amino acid dipeptide derivs. as cell adhesion inhibitors)

IT **136466-51-8 150525-67-0** 187345-00-2
187738-30-3 414866-20-9
RL: PRP (Properties)
(unclaimed sequence; prepn. of dipeptide derivs. as cell adhesion inhibitors)

RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L44 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2002 ACS
AN 2000:772477 HCAPLUS
DN 133:334056
TI Method for the treatment of fibrosis using an antagonist of the integrin alpha-4 subunit
IN Gotwals, Philip; **Lobb, Roy R.**
PA **Biogen, Inc., USA**
SO PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM A61K039-395
ICS A61P011-00; A61P037-00
CC 15-3 (Immunochemistry)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000064474	A1	20001102	WO 2000-US10781	20000421
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1173201	A1	20020123	EP 2000-926238	20000421
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	BR 2000010669	A	20020219	BR 2000-10669	20000421
	NO 2001005122	A	20011221	NO 2001-5122	20011019
PRAI	US 1999-130847P	P	19990422		
	US 1999-137214P	P	19990601		
	WO 2000-US10781	W	20000421		

AB Disclosed is a method of treating fibrosis in a human or animal subject. The method comprises administering to the subject an effective amt. of an antagonist, i.e. antibody, to VLA-4 integrin or fragment thereof.

ST fibrosis integrin alpha4 VLA4 antibody fragment
IT Integrins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(LPAM-1 (lymphocyte Peyer's patch high endothelial venule adhesion mol. 1); integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Nucleic acids
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(anti-integrin .alpha.4 antibody-encoding; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Fusion proteins (chimeric proteins)
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antibody; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Body fluid
(bronchoalveolar lavage fluid; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Lung, disease
(fibrosis; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Immunoglobulins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(fragments; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Animal
Fibrosis
Leukocyte
(integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Ligands
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(integrin .alpha.4; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Integrins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(.alpha.4; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT Integrins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(.alpha.4.beta.1; integrin .alpha.4 antibody or antagonist for treatment of fibrosis)
IT 304678-50-0
RL: PRP (Properties)
(Unclaimed; method for the treatment of fibrosis using an antagonist of the integrin alpha-4 subunit)
IT **136466-51-8 150525-67-0** 187345-00-2
RL: PRP (Properties)
(unclaimed sequence; method for the treatment of fibrosis using an antagonist of the integrin alpha-4 subunit)
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L44 ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2002 ACS
AN 2000:683175 HCAPLUS
DN 134:4000
TI Differential Induction of Gelatinase B (MMP-9) and Gelatinase A (MMP-2) in T Lymphocytes upon .alpha.4.beta.1-Mediated Adhesion to VCAM-1 and the CS-1 Peptide of Fibronectin
AU Yakubenko, Valentin P.; **Lobb, Roy R.**; Plow, Edward F.; Ugarova, Tatiana P.
CS Joseph J. Jacobs Center for Thrombosis and Vascular Biology, Department of Molecular Cardiology, Lerner Research Institute of the Cleveland Clinic Foundation, Cleveland, OH, 44195, USA
SO Experimental Cell Research (2000), 260, 73-84
CODEN: ECREAL; ISSN: 0014-4827
PB Academic Press
DT Journal
LA English
CC 15-10 (Immunochemistry)
AB Integrin .alpha.4.beta.1 on the surface of T lymphocytes interacts with vascular cell adhesion mol.-1 (VCAM-1) and fibronectin during migration of lymphocytes from the blood to sites of inflammation. Migrating lymphocytes actively modify their environment through a no. of mechanisms including proteolysis of the extracellular matrix by matrix metalloproteinases (MMP) synthesized by the cells. In this study, expression of MMP upon .alpha.4.beta.1-mediated adhesion of leukocytes to two major ligands, the IIICS-1 domain of fibronectin and VCAM-1, has been examd. Adhesion of T lymphoblastoid Jurkat cells to the CS-1 peptide induced expression of mRNA for two MMPs, gelatinase A (MMP-2) and gelatinase B (MMP-9). As evaluated by relative RT-PCR and Northern blot analyses, the level of mRNA was upregulated about 4- to 5-fold for both MMPs compared to control cells maintained in suspension. With time, both enzymes were detected in conditioned media and inside the cells, and their identities were verified by Western blotting and gelatin zymog. Adhesion of Jurkat cells to the second major .alpha.4.beta.1 ligand, VCAM-1, upregulated mRNA for MMP-2 (3.5-fold) and failed to induce expression of mRNA for MMP-9. Accordingly, only MMP-2 protein was detected in conditioned media of cells adherent to VCAM-1. Occupancy of .alpha.4.beta.1 on the surface of suspended cells with sol. CS-1 peptide or VCAM-1 did not upregulate synthesis and release of MMPs. A similar pattern of induction of MMPs after adhesion to CS-1 and VCAM-1 was obsd. in T lymphocytes isolated from human blood. These results demonstrate that adhesion of T lymphocytes through .alpha.4.beta.1 to different ligands, which bind to similar or overlapping sites in the integrin, induces intracellular events leading to distinct patterns of MMPs biosynthesis. (c) 2000 Academic Press.
ST T lymphocyte adhesion integrin VCAM fibronectin gelatinase
IT Cell adhesion molecules
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(VCAM-1; differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)
IT T cell (lymphocyte)
(adhesion; differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)
IT Inflammation
Signal transduction, biological
(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)
IT mRNA

RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT Fibronectins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT Integrins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(.alpha.4.beta.1; differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT **107978-77-8**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

IT 146480-35-5, Gelatinase A 146480-36-6, Gelatinase B
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(differential induction of gelatinase B (MMP-9) and gelatinase A (MMP-2) in T lymphocytes upon .alpha.4.beta.1-mediated adhesion to VCAM-1 and CS-1 peptide of fibronectin)

RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L44 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 2002 ACS
AN 1999:216816 HCAPLUS
DN 130:321465
TI Comparative genomes of Chlamydia pneumoniae and C. trachomatis
AU Kalman, Sue; Mitchell, Wayne; Marathe, Rekha; Lammel, Claudia; Fan, Jun; Hyman, Richard W.; Olinger, Lynn; Grimwood, Jane; Davis, Ronald W.; Stephens, Richard S.
CS Stanford DNA Sequencing and Technology, Center, Stanford University, Stanford, CA, 94305, USA
SO Nature Genetics (1999), 21(4), 385-389
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal
LA English
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 7, 10
AB Chlamydia are obligate intracellular eubacteria that are phylogenetically sepd. from other bacterial divisions. C. trachomatis and C. pneumoniae are both pathogens of humans but differ in their tissue tropism and spectrum of diseases. C. pneumoniae is a newly recognized species of Chlamydia that is a natural pathogen of humans, and causes pneumonia and bronchitis. In the United States, approx. 10% of pneumonia cases and 5% of bronchitis cases are attributed to C. pneumoniae infection. Chronic disease may result following respiratory-acquired infection, such as reactive airway disease, adult-onset **asthma** and potentially lung cancer. In addn., C. pneumoniae infection has been assocd. with atherosclerosis. C. trachomatis infection causes trachoma, an ocular

infection that leads to blindness, and sexually transmitted diseases such as pelvic inflammatory disease, chronic pelvic pain, ectopic pregnancy and epididymitis. Although relatively little is known about C. trachomatis biol., even less is known concerning C. pneumoniae. Comparison of the C. pneumoniae genome with the C. trachomatis genome will provide an understanding of the common biol. processes required for infection and survival in mammalian cells. Genomic differences are implicated in the unique properties that differentiate the two species in disease spectrum. Anal. of the 1,230,230-nt C. pneumoniae genome revealed 214 protein-coding sequences not found in C. trachomatis, most without homologues to other known sequences. Prominent comparative findings include expansion of a novel family of 21 sequence-variant outer-membrane proteins, conservation of a type-III secretion virulence system, three serine/threonine protein kinases and a pair of parologous phospholipase-D-like proteins, addnl. purine and biotin biosynthetic capability, a homolog for arom. amino acid (tryptophan) hydroxylase and the loss of tryptophan biosynthesis genes.

ST sequence Chlamydia pneumoniae genome; species difference Chlamydia trachomatis pneumoniae genome sequence comparison

IT Proteins, specific or class
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(Pmp (polymorphic membrane protein); comparative genomes of Chlamydia pneumoniae and C. trachomatis)

IT Chlamydia trachomatis
Genome
(comparative genomes of Chlamydia pneumoniae and C. trachomatis)

IT Chlamydia pneumoniae
(genomic sequence of; comparative genomes of Chlamydia pneumoniae and C. trachomatis)

IT DNA sequences
Protein sequences
(of Chlamydia pneumoniae)

IT Gene, microbial
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(pmp; comparative genomes of Chlamydia pneumoniae and C. trachomatis)

IT 75432-95-0, Arom. amino acid oxidase
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(C. pneumoniae gene for; comparative genomes of Chlamydia pneumoniae and C. trachomatis)

IT 135946-71-3, Protein MOMP (Chlamydia pneumoniae strain IOL-207 precursor reduced) 136363-37-6, Protein (Chlamydia pneumoniae clone pLC3 71.5-kilodalton reduced) 145170-64-5, Chaperonin 10 (Chlamydia pneumoniae strain AR-39 gene groES) 172279-76-4 172313-16-5 219303-77-2 223700-67-2 223700-68-3 223700-69-4 223700-70-7 223700-71-8 223700-72-9 223700-73-0 223700-74-1 223700-75-2 223700-76-3 223700-77-4 223700-78-5, Protein (Chlamydia pneumoniae gene dsbG) 223700-79-6 223700-80-9 223700-81-0 223700-82-1 223700-83-2 223700-84-3 223700-85-4 223700-86-5 223700-87-6 223700-88-7 223700-89-8, Protein (Chlamydia pneumoniae gene yggF) 223700-90-1 223700-91-2 223700-92-3 223700-93-4 223700-94-5 223700-95-6 223700-96-7 223700-97-8 223700-99-0 223701-00-6 223701-01-7, Protein (Chlamydia pneumoniae gene ydhO) 223701-02-8 223701-03-9 223701-14-2 223701-15-3 223701-16-4 223701-17-5 223701-18-6 223701-19-7 223701-20-0 223701-21-1 223701-22-2 223701-23-3 223701-24-4 223701-25-5 223701-26-6 223701-27-7 223701-28-8 223701-29-9 223701-30-2 223701-32-4 223701-33-5, Protein (Chlamydia pneumoniae gene ydaO) 223701-34-6 223701-35-7 223701-39-1 223701-40-4 223701-42-6 223701-43-7 223701-44-8 223701-45-9 223701-47-1 223701-48-2 223701-49-3 223701-50-6 223701-51-7 223701-52-8 223701-53-9 223701-54-0 223701-56-2, Protein (Chlamydia pneumoniae gene yqeV) 223701-57-3, Protein (Chlamydia

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; comparative genomes of Chlamydia pneumoniae and
C. trachomatis)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; comparative genomes of Chlamydia pneumoniae and C. trachomatis)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; comparative genomes of Chlamydia pneumoniae and
C. trachomatis)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; comparative genomes of Chlamydia pneumoniae and C. trachomatis)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; comparative genomes of Chlamydia pneumoniae and C. trachomatis)

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; comparative genomes of Chlamydia pneumoniae and C. trachomatis)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Altschul, S; Nucleic Acids Res 1997, V25, P3389 HCAPLUS
(2) Campbell, L; J Clin Microbiol 1987, V25, P1911 HCAPLUS
(3) Emre, U; J Infect Dis 1995, V172, P265 MEDLINE
(4) Fong, I; J Clin Microbiol 1997, V35, P48 MEDLINE
(5) Grayston, J; Int J Syst Bacteriol 1989, V39, P88
(6) Hahn, D; Epidemiol Infect 1996, V117, P513 MEDLINE
(7) Kuo, C; Arterioscler Thromb 1993, V13, P1501 MEDLINE
(8) Kuo, C; Clin Microbiol Rev 1995, V8, P451 MEDLINE
(9) Kuo, C; J Infect Dis 1993, V167, P841 MEDLINE
(10) Kuo, C; Proc Natl Acad Sci USA 1995, V92, P6911 HCAPLUS
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(18) Rockey, D; Mol Microbiol 1995, V15, P617 HCAPLUS
(19) Salzberg, S; Nucleic Acids Res 1997, V26, P544
(20) Schachter, J; West J Med 1990, V153, P523 MEDLINE
(21) Stephens, R; Infect Agents Dis 1992, V1, P279 MEDLINE
(22) Stephens, R; Science 1998, V282, P754 HCAPLUS
(23) Thompson, J; Nucleic Acids Res 1994, V22, P4673 HCAPLUS

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STRUCTURE FILE UPDATES: 7 JUN 2002 HIGHEST RN 427375-75-5
DICTIONARY FILE UPDATES: 7 JUN 2002 HIGHEST RN 427375-75-5

TSCA INFORMATION NOW CURRENT THROUGH January 7, 2002

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS

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Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

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L56  ANSWER 1 OF 4  REGISTRY  COPYRIGHT 2002 ACS
RN   223737-50-6  REGISTRY
CN   L-Lysine, L-methionyl-L-.alpha.-aspartyl-L-leucyl-L-glutaminyl-L-alanyl-L-
     phenylalanyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-
     valyl-L-glutaminylglycyl-L-methionyl-L-leucyl-L-threonyl-L-.alpha.-
     aspartyl-L-glutaminyl-L-arginyl-L-lysyl-L-histidyl-L-isoleucyl-L-
     glutaminyl-L-methionyl-L-leucyl-L-histidyl-L-lysyl-L-histidyl-L-
     asparaginyl-L-seryl-L-isoleucyl-L-.alpha.-glutamyl-L-isoleucyl-L-
     phenylalanyl-L-leucyl-L-seryl-L-asparaginyl-L-methionyl-L-valyl-L-valyl-L-
     .alpha.-glutamyl-L-valyl-L-lysyl-L-leucyl-L-phenylalanyl-L-phenylalanyl-L-
     lysyl-L-threonyl-L-leucyl- (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AE001651-derived protein GI 4376987
CN   GenBank AP002547-derived protein GI 8979057
CN   Protein (Chlamydia pneumoniae gene CPn0685)
CN   Protein (Chlamydia pneumoniae strain J138 gene CPj0685)
FS   PROTEIN SEQUENCE
SQL  50

SEQ      1 MDLQAFEILD VQGMLTDQRK HIQMLHKHNS IEIFLSNMVV EVKLFFKTLK
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HITS AT:   7-11
MF   C270 H436 N70 O73 S4
CI   MAN
SR   CA
LC   STN Files:   CA, CAPLUS
                2 REFERENCES IN FILE CA (1967 TO DATE)
                2 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE   1:  134:232463

REFERENCE   2:  130:321465

L56  ANSWER 2 OF 4  REGISTRY  COPYRIGHT 2002 ACS
RN   223710-22-3  REGISTRY
CN   Synthetase, methionyl-transfer ribonucleate (Chlamydia pneumoniae gene
     metG) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AE001598-derived protein GI 4376385
CN   Methionyl-tRNA synthetase (Chlamydia pneumoniae gene metG)
FS   PROTEIN SEQUENCE
SQL  551

SEQ      1 MPQKVLITSA LPYANGPLHF GHIAGVYLPA DVYARFRRLL GDDVLYICGS
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       101 HAELVQDFYS QLKASGLIEN RISEQLYSEQ EQRFLADRYV EGTCPRCGFD
       151 HARGDECQSC GADYEAIDLI GPKSKISGVE LVKKETEHSY FLLDRMKDAL
       201 LSFIQGCYLP DHVRKFVVDY IEHVRSRAIT RDLSWGIPVP DFPGKVFYVW
       251 FDAPIGYISG TMEWAASQGN PDEWKRFWLE DGVEYVQFIG KDNLPFHSVV
       301 FPAMELGQKL DYKKVDALVV SEFYLLEGRQ FSKSEGNYVD MDKFLSSYSL
       351 DKLRYVLAAT APETSDSEFT FLDFKTRCNS ELVGKFGNFI NRVLAFAEKN
       401 HYDKLSYHSV VLEDSDRAFL EEARQLVRDA EKCYREYSLR KATSVIMSLA
       451 ALGNVYFNQQ APWKLLKEGT RERVEAILFC ACYCQKLLAL ISYPIIPESA
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MF   Unspecified
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CI MAN
SR CA
LC STN Files: CA, CAPLUS
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:321465

L56 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2002 ACS
RN **136466-51-8** REGISTRY
CN L-Threonine, L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl- (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN L-Threonine, N-[N-[1-[N-[N-[N-(N-L-.alpha.-glutamyl-L-isoleucyl)-L-leucyl]-L-.alpha.-aspartyl]-L-valyl]-L-prolyl]-L-seryl]-
OTHER NAMES:
CN 1: PN: US6376538 SEQID: 1 unclaimed sequence
CN 1: PN: WO0064474 PAGE: 19 unclaimed sequence
CN 24: PN: WO0004941 PAGE: 32 claimed sequence
CN 458: PN: WO0069900 SEQID: 1143 unclaimed sequence
CN 47: PN: US6051429 SEQID: 48 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 8

SEQ 1 EILDVPST
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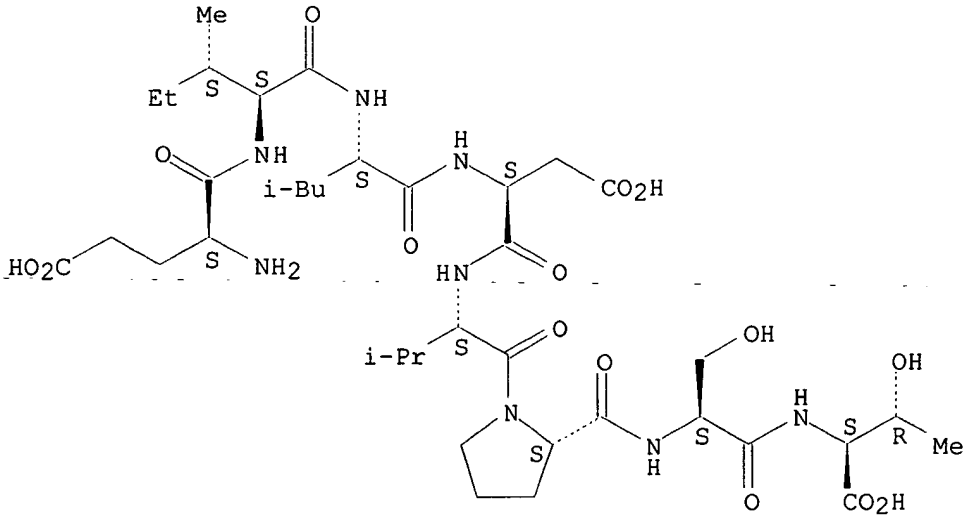
MF C38 H64 N8 O15
CI COM
SR CA
LC STN Files: CA, CAPLUS, CHEMCATS, TOXCENTER, USPATFULL

Absolute stereochemistry.



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2 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
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REFERENCE 2: 136:325828

REFERENCE 3: 134:21425

REFERENCE 4: 133:334056

REFERENCE 5: 133:221490

REFERENCE 6: 132:289590

REFERENCE 7: 132:142003

REFERENCE 8: 131:175085

REFERENCE 9: 131:175083

REFERENCE 10: 130:48275

L56 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2002 ACS
RN **107978-77-8** REGISTRY
CN L-Threonine, L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-leucyl-L-prolyl-L-glutaminyl-L-leucyl-L-valyl-L-threonyl-L-leucyl-L-prolyl-L-histidyl-L-prolyl-L-asparaginyl-L-leucyl-L-histidylglycyl-L-prolyl-L-.alpha.-glutamyl-L-isoleucyl-L-leucyl-L-.alpha.-aspartyl-L-valyl-L-prolyl-L-seryl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 15: PN: US6013628 SEQID: 15 claimed protein
CN 37: PN: US6051429 SEQID: 17 unclaimed sequence
CN 3: PN: US20020012942 SEQID: 3 claimed protein
CN 3: PN: WO0187071 SEQID: 4 unclaimed sequence
CN 4: PN: US20020012942 SEQID: 4 claimed protein
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 25

SEQ 1 DELPQLVTLP HPNLHGPEIL DVPST
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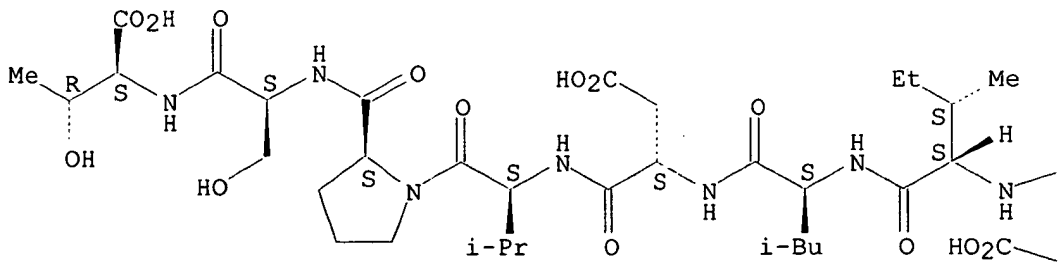
HITS AT: 18-22
MF C123 H195 N31 O39
SR CA
LC STN Files: CA, CANCERLIT, CAPLUS, CHEMCATS, MEDLINE, TOXCENTER, USPATFULL

Absolute stereochemistry.

PAGE 1-A



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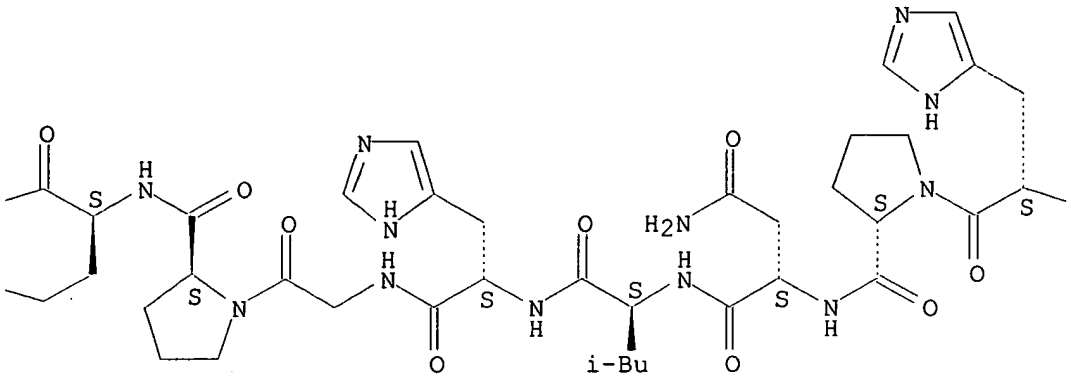

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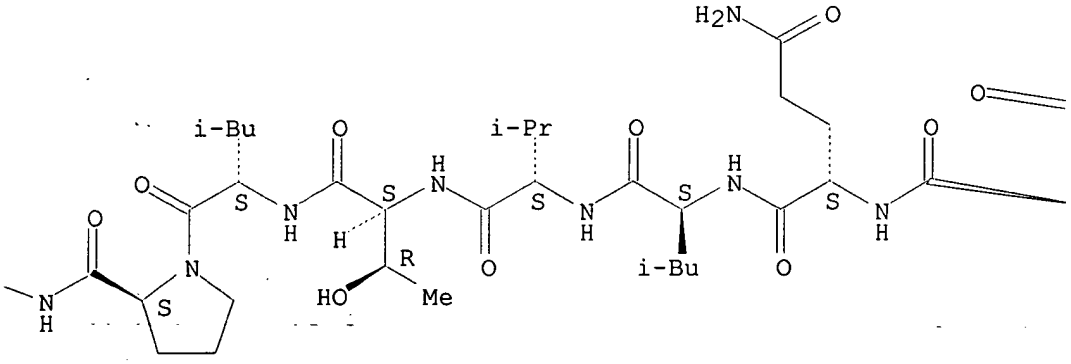

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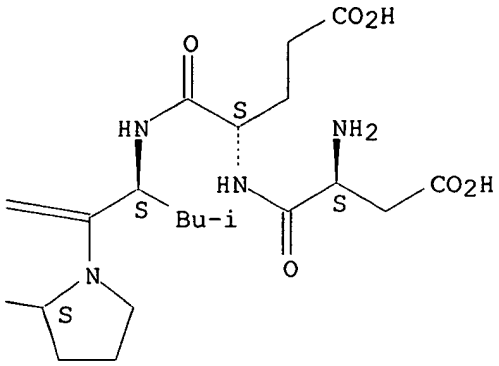

32 REFERENCES IN FILE CA (1967 TO DATE)
3 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
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REFERENCE 1: 136:336176

REFERENCE 2: 136:145279

REFERENCE 3: 135:366749

REFERENCE 4: 134:4000

REFERENCE 5: 133:261094

REFERENCE 6: 132:289590

REFERENCE 7: 132:88194

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REFERENCE 9: 131:175083

REFERENCE 10: 131:125484

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CA INDEXING COPYRIGHT (C) 2002 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 08:27:50 ON 10 JUN 2002
CA INDEXING COPYRIGHT (C) 2002 AMERICAN CHEMICAL SOCIETY (ACS)

=> d bib abs hitrn tot l50

L50 ANSWER 1 OF 13 USPATFULL
AN 2002:88519 USPATFULL
TI Cell adhesion inhibitors
IN Adams, Steven P., Andover, MA, United States
Lin, Ko-Chung, Lexington, MA, United States
Lee, Wen-Cherng, Lexington, MA, United States
Castro, Alfredo C., Woburn, MA, United States
Zimmerman, Craig N., Somerville, MA, United States
Hammond, Charles E., Burlington, MA, United States
Liao, Yu-Sheng, Lexington, MA, United States
Cuervo, Julio Hernan, Arlington, MA, United States

Singh, Juswinder, Malden, MA, United States
PA Biogen, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6376538 B1 20020423
WO 9622966 19960801
AI US 1997-875321 19970919 (8)
WO 1996-US1349 19960118
19970919 PCT 371 date
RLI Continuation-in-part of Ser. No. US 1995-376372, filed on 23 Jan 1995, now patented, Pat. No. US 6306840
DT Utility
FS GRANTED
EXNAM Primary Examiner: Aulakh, Charanjit S.
LREP Fish & Richardson P.C.
CLMN Number of Claims: 56
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 4655
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel compounds that are useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compounds and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compounds and pharmaceutical compositions of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **136466-51-8 150525-67-0 187738-30-3**
(unclaimed sequence; prepn. of dipeptide derivs. as cell adhesion inhibitors)

L50 ANSWER 2 OF 13 USPATFULL
AN 2002:84902 USPATFULL
TI Nucleic acids, proteins and antibodies
IN Rosen, Craig A., Laytonsville, MD, UNITED STATES
Ruben, Steven M., Olney, MD, UNITED STATES
PI US 2002044941 A1 20020418
AI US 2001-925302 A1 20010810 (9)
RLI Continuation-in-part of Ser. No. WO 2000-US5918, filed on 8 Mar 2000, UNKNOWN
PRAI US 1999-124270P 19990312 (60)
DT Utility
FS APPLICATION
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 21121
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel lung cancer related polynucleotides, the polypeptides encoded by these polynucleotides herein collectively referred to as "lung cancer antigens," and antibodies that immunospecifically bind these polypeptides, and the use of such lung cancer polynucleotides, antigens, and antibodies for detecting, treating, preventing and/or prognosing disorders of the lung, including, but not limited to, the presence of lung cancer and lung cancer metastases. More specifically, isolated lung cancer nucleic acid molecules are provided encoding novel lung cancer polypeptides. Novel lung cancer polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human lung cancer polynucleotides, polypeptides, and/or antibodies. The invention further relates to

diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the lung, including lung cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The invention further relates to methods and/or compositions for inhibiting or promoting the production and/or function of the polypeptides of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **409148-95-4P**
(amino acid sequence; human nucleic acids and their encoded proteins and antibodies assocd. with lung cancer)

L50 ANSWER 3 OF 13 USPATFULL
AN 2002:78727 USPATFULL
TI INTEGRIN-TARGETING VECTORS HAVING TRANSFECTION ACTIVITY
IN HART, STEPHEN L., LONDON, UNITED KINGDOM
PI US 2002042384 A1 20020411
AI US 1999-424656 A1 19991129 (9)
WO 1998-GB1577 19980529
PRAI GB 1997-11115 19970529
DT Utility
FS APPLICATION
LREP NIXON & VANDERHYE, 1100 NORTH GLEBE ROAD, 8TH FLOOR, ARLINGTON, VA, 222014714
CLMN Number of Claims: 55
ECL Exemplary Claim: 1
DRWN 9 Drawing Page(s)
LN.CNT 1527
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A complex that comprises (i) a nucleic acid, (ii) an integrin-binding component, for example, an integrin-binding peptide, (iii) a polycationic nucleic acid-binding component, for example, oligolysine, and (iv) a lipid component, for example, a cationic liposome, has transfection activity.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **216964-48-6**
(integrin-targeting vectors having transfection activity)

L50 ANSWER 4 OF 13 USPATFULL
AN 2001:93479 USPATFULL
TI Cell adhesion inhibitors
IN Lin, Ko-Chung, Lexington, MA, United States
Adams, Steven P., Andover, MA, United States
Castro, Alfredo C., Woburn, MA, United States
Zimmerman, Craig N., Somerville, MA, United States
Cuervo, Julio Hernan, Cambridge, MA, United States
Lee, Wen-Cherng, Lexington, MA, United States
Hammond, Charles E., Burlington, MA, United States
Carter, Mary Beth, Belmont, MA, United States
Almquist, Ronald G., Lexington, MA, United States
PA Biogen, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6248713 B1 20010619
AI US 1995-498237 19950711 (8)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Celsa, Bennett
LREP Fish & Richardson P.C.
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN No Drawings

LN.CNT 2501
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel compounds that are useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compounds and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compounds and pharmaceutical compositions of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **187738-30-3DP**, conjugate with bovine serum albumin
(prepn. of peptide derivs. as cell adhesion inhibitors)
IT **187738-30-3P**
(prepn. of peptide derivs. as cell adhesion inhibitors)

L50 ANSWER 5 OF 13 USPATFULL
AN 2001:79133 USPATFULL
TI Cell adhesion inhibitors
IN Lin, Ko-Chung, Lexington, MA, United States
Adams, Steven P., Andover, MA, United States
Castro, Alfredo C., Woburn, MA, United States
Zimmerman, Craig N., Topsfield, MA, United States
Cuervo, Julio Hernan, Arlington, MA, United States
Lee, Wen-Cherng, Lexington, MA, United States
Hammond, Charles E., Burlington, MA, United States
Carter, Mary Beth, Belmont, MA, United States
Almquist, Ronald G., Lexington, MA, United States
PA Biogen, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6239108 B1 20010529
WO 9703094 19970130
AI US 1998-983391 19980810 (8)
WO 1996-US11570 19960711
19980810 PCT 371 date
19980810 PCT 102(e) date
DT Utility
FS Granted
EXNAM Primary Examiner: Davenport, Avis M.
LREP Fish & Richardson P.C.
CLMN Number of Claims: 49
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 3146
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel compounds that are useful for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. This invention also relates to pharmaceutical formulations comprising these compounds and methods of using them for inhibition and prevention of cell adhesion and cell adhesion-mediated pathologies. The compounds and pharmaceutical compositions of this invention can be used as therapeutic or prophylactic agents. They are particularly well-suited for treatment of many inflammatory and autoimmune diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **187738-30-3DP**, conjugate with bovine serum albumin
(prepn. of peptide derivs. as cell adhesion inhibitors)
IT **187738-30-3P**
(prepn. of peptide derivs. as cell adhesion inhibitors)

L50 ANSWER 6 OF 13 USPATFULL
AN 2000:98458 USPATFULL
TI Compounds that inhibit the binding of integrins to their receptors

IN Scott, Ian L., Albany, NY, United States
Raju, Bore G., Fremont, CA, United States
Biediger, Ronald J., Houston, TX, United States
Grabbe, Vanessa O., Sugar Land, TX, United States
Kassir, Jamal, Houston, TX, United States
Keller, Karin M., Houston, TX, United States
Kogan, deceased, Timothy P., late of Sugar Land, TX, United States by Patricia Woodard Kogan, executrix
Lin, Shuqun, Huntingdon Valley, PA, United States
Market, Robert V., Pearland, TX, United States
PA Texas Biotechnology Corporation, Inc., Houston, TX, United States (U.S. corporation)
PI US 6096773 20000801
AI US 1999-292459 19990415 (9)
PRAI US 1998-82019P 19980416 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: McKane, Joseph K.; Assistant Examiner: Solola, Taofiq A.
LREP Rockey, Milnamow & Katz, Ltd.
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1469
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for the inhibition of the binding of .alpha..sub.4 .beta..sub.1 integrin to its receptors, for example VCAM-1 (vascular cell adhesion molecule-1) and fibronectin; compounds that inhibit this binding; pharmaceutically active compositions comprising such compounds; and the use of such compounds either as above, or in formulations for the control or prevention of diseases states in which .alpha..sub.4 .beta..sub.1 is involved.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **247094-59-3**
(ovalbumin conjugates; compds. that inhibit binding of integrins to receptors such as VCAM-1 and fibronectin)

L50 ANSWER 7 OF 13 USPATFULL
AN 2000:27952 USPATFULL
TI Fibronectin adhesion inhibitors
IN Dutta, Anand Swaroop, Macclesfield, United Kingdom
PA Zeneca Limited, London, United Kingdom (non-U.S. corporation)
PI US 6034056 20000307
WO 9620216 19960704
AI US 1997-860248 19970624 (8)
WO 1995-GB2992 19951221
19970624 PCT 371 date
19970624 PCT 102(e) date
PRAI GB 1994-26254 19941224
GB 1995-5905 19950324
GB 1995-13904 19950707
DT Utility
FS Granted
EXNAM Primary Examiner: Tsang, Cecilia J.
LREP Phillsbury Madison & Sutro, LLPIntellectual Property Group
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN 16 Drawing Figure(s); 22 Drawing Page(s)
LN.CNT 3750
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Cyclic peptides of formula (1): ##STR1## Wherein: AA1 is an L or D amino acid selected from Ile and Leu or amino acid analogue thereof; AA2 is an

L amino acid selected from Leu or amino acids analogue thereof; AA3 is an L amino acid selected from Asp or amino acid analogue thereof containing a carboxy group in its side chain; AA4 is an L amino acid selected from Val or amino acid analogue thereof and; LINKER represents a linking moiety for linking N terminus of AA1 to C terminus of AA4 to form a cyclic peptide containing a heterocyclic ring having 17 to 30 members. The cyclic peptides inhibit the interaction of vascular cell adhesion molecule-1 and fibronectin with integrin very late antigen 4 and have therapeutic applications such as in rheumatoid arthritis or multiple sclerosis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **180575-30-8P 180575-31-9P 180575-32-0P**
180575-33-1P
(prepn. of cyclopeptide fibronectin adhesion inhibitors for treatment of rheumatoid arthritis and multiple sclerosis)

L50 ANSWER 8 OF 13 USPATFULL
AN 1999:163664 USPATFULL
TI Inhibitors of leukocyte adhesion
IN Thorsett, Eugene D., Moss Beach, CA, United States
Yednock, Theodore A., Fairfax, CA, United States
Pleiss, Michael A., Fremont, CA, United States
PA Elan Pharmaceuticals, Inc., South San Francisco, CA, United States (U.S. corporation)
PI US 6001809 19991214
AI US 1995-467580 19950606 (8)
RLI Continuation-in-part of Ser. No. US 1994-273055, filed on 11 Jul 1994, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Tsang, Cecilia J.; Assistant Examiner: Delacroix-Muirheid, C.
LREP Stratford, Carol A., Duvall, Jean M.Burns, Doane, Swecker & Mathis, LLP
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 2132
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides peptides which block cellular adhesion mediated by VLA-4. The peptides can be used to treat a number of inflammatory diseases, in particular, inflammatory brain disorders.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **174962-82-4 174962-83-5**
(anti-inflammatory peptide inhibitors of leukocyte adhesion mediated by VLA-4)

L50 ANSWER 9 OF 13 USPATFULL
AN 1999:92778 USPATFULL
TI CS-1 peptidomimetics, compositions and methods of using the same
IN Arrhenius, Thomas S., San Diego, CA, United States
Elices, Mariano J., San Diego, CA, United States
Gaeta, Federico C. A., Olivenhain, CA, United States
PA Cytel Corporation, San Diego, CA, United States (U.S. corporation)
PI US 5936065 19990810
AI US 1995-462424 19950605 (8)
RLI Continuation-in-part of Ser. No. US 1994-349024, filed on 2 Dec 1994, now abandoned which is a continuation-in-part of Ser. No. US 1993-164101, filed on 6 Dec 1993, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Tsang, Cecilia J.; Assistant Examiner: Lukton, David

LREP Campbell & Flores LLP
CLMN Number of Claims: 2
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 3625
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention contemplates a compound defined by the following formula: ##STR1## that inhibits the binding between the VLA-4 and the fibronectin CS-1 compound. Pharmaceutical compositions containing a contemplated compound and methods for treating immunoinflammatory conditions using the compound are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **126235-03-8 150525-67-0 236100-99-5**
236101-00-1 236101-01-2 236101-02-3
236101-04-5 236101-05-6
(fibronectin CS-1 peptidomimetics for inhibiting binding of CS-1 to VLA-4 and for treating immunoinflammatory conditions)

L50 ANSWER 10 OF 13 USPATFULL
AN 1999:19112 USPATFULL
TI Cyclic CS-1 peptidomimetics, compositions and methods of using same
IN Arrhenius, Thomas S., San Diego, CA, United States
Tempczyk, Anna, San Diego, CA, United States
Elices, Mariano J., San Diego, CA, United States
Zheng, Zhong-Li, Lexington, MA, United States
PA Cytel Corporation, San Diego, CA, United States (U.S. corporation)
PI US 5869448 19990209
AI US 1995-519109 19950825 (8)
RLI Continuation-in-part of Ser. No. US 1995-483077, filed on 7 Jun 1995 which is a continuation-in-part of Ser. No. US 1994-296241, filed on 25 Aug 1994, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Russel, Jeffrey E.
LREP Campbell & Flores LLP
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 1 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 2088
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention contemplates a cyclic peptide that inhibits the binding between the VLA-4 receptor expressed on inflammatory leukocytes and the fibronectin CS-1 peptide expressed on endothelial cells that are involved in immunoinflammatory disease states. Pharmaceutical compositions containing a contemplated cyclic peptide and processes for treating immunoinflammatory conditions using a binding-inhibitory cyclic peptide are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **126235-03-8P**
(cyclic peptides inhibiting binding of VLA4 receptor and fibronectin CS-1 peptide, compns., and methods of treatment of immunoinflammatory conditions)
IT **107978-77-8**
(cyclic peptides inhibiting binding of VLA4 receptor and fibronectin CS-1 peptide, compns., and methods of treatment of immunoinflammatory conditions)

L50 ANSWER 11 OF 13 USPATFULL
AN 1998:115706 USPATFULL
TI Cyclic CS-1 peptidomimetics, compositions and methods of using same
IN Arrhenius, Thomas S., San Diego, CA, United States

Elices, Mariano J., San Diego, CA, United States
Tempczyk, Anna, San Diego, CA, United States
Zheng, Zhong-Li, Lexington, MA, United States
PA Cytel Corporation, San Diego, CA, United States (U.S. corporation)
PI US 5811391 19980922
AI US 1995-483077 19950607 (8)
RLI Continuation-in-part of Ser. No. US 1994-296241, filed on 25 Aug 1994, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Russel, Jeffrey E.
LREP Campbell & Flores LLP
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN 1 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 1919
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention contemplates a cyclic peptide that inhibits the binding between the VLA-4 receptor expressed on inflammatory leukocytes and the fibronectin CS-1 peptide expressed on endothelial cells that are involved in immunoinflammatory disease states. Pharmaceutical compositions containing a contemplated cyclic peptide and processes for treating immunoinflammatory conditions using a binding-inhibitory cyclic peptide are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **126235-03-8P**
(prepn. of cyclic CS-1 peptidomimetics and their compns.)

L50 ANSWER 12 OF 13 USPATFULL
AN 1998:30693 USPATFULL
TI Inhibition of lymphocyte adherence with .alpha.4.beta.1-specific antibodies
IN Wayner, Elizabeth A., St. Paul, MN, United States
PA Fred Hutchinson Cancer Research Center, Seattle, WA, United States (U.S. corporation)
PI US 5730978 19980324
AI US 1994-338282 19941114 (8)
RLI Continuation of Ser. No. US 1991-814873, filed on 24 Dec 1991, now abandoned which is a continuation-in-part of Ser. No. US 1989-402389, filed on 1 Sep 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Feisee, Lila; Assistant Examiner: Gambel, Phillip
LREP Townsend and Townsend and Crew LLP
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 31 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 2876
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to a method for inhibiting the adhesion of one cell to another comprising interfering with the interaction between the extracellular matrix receptor and its ligand.

The invention is based upon the discovery that the .alpha.4.beta.1 extracellular matrix receptor promotes adhesion of lymphocytes to endothelial cells via attachment to a defined peptide sequence. Prior to the present invention, the ligand of the .alpha.4.beta.1 receptor had not been identified, nor had the function of the .alpha.4.beta.1 receptor in lymphocyte attachment been known. By preventing the interaction between the .alpha.4.beta.1 receptor and its ligands using antibodies or defined peptide sequences, the present invention enables, for the first time, specific intervention in the migration of

lymphocytes through the vascular endothelium and into tissues. The present invention, therefore, has particular clinical utility in suppression of the immune response; in various specific embodiments of the invention, the adherence of lymphocytes to endothelium may be inhibited systemically, or may, alternatively, be localized to particular tissues or circumscribed areas. Accordingly, the present invention provides for treatment of diseases involving autoimmune responses as well as other chronic or relapsing activations of the immune system, including allergy, **asthma**, and chronic inflammatory skin conditions.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **136466-51-8**
(binding of, or fragment or homologous sequence of, to .alpha.4.beta.1 extracellular matrix receptor for inhibition of lymphocyte adhesion to endothelial cell)
IT **126235-03-8 128701-34-8**
(fibronectin-derived peptide, effect of, on lymphocyte adhesion to endothelial cell, .alpha.4.beta.1 extracellular matrix receptor in relation to)

L50 ANSWER 13 OF 13 USPATFULL
AN 96:34108 USPATFULL
TI Process to inhibit binding of the integrin .alpha..sub.4 62 .sub.1 to VCAM-1 or fibronectin and linear peptides therefor
IN Kogan, Timothy P., Sugar Land, TX, United States
Ren, Kaijun, Sugar Land, TX, United States
Vanderslice, Peter, Houston, TX, United States
Beck, Pamela J., Houston, TX, United States
PA Texas Biotechnology Corporation, Houston, TX, United States (U.S. corporation)
PI US 5510332 19960423
AI US 1994-271830 19940707 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Chan, Christina Y.; Assistant Examiner: Prickril, Benet
LREP Dressler, Goldsmith, Shore & Milnamow, Ltd.
CLMN Number of Claims: 15
ECL Exemplary Claim: 1,5
DRWN No Drawings
LN.CNT 1344
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is directed to an isolated and purified peptide comprising the LDV domain of the CSI peptide sequence or single amino acid substitutent analog thereof. A preferred peptide has the amino acid residue sequences shown in SEQ ID NOs:8-14, 17-23, 25, 28, and 51. The present invention is further directed to a process of inhibiting the binding of .alpha..sub.4 .beta..sub.1 integrin to a protein such as VCAM-1 or fibronectin comprising exposing a cell that expresses .alpha..sub.4 .beta..sub.1 integrin to the protein in the presence of an effective inhibiting amount of such a peptide. The present invention is still further directed to a pharmaceutical composition comprising a peptide of SEQ ID NO:8-102.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **159680-18-9DP**, conjugates with polyethylene glycol
176955-06-9DP, conjugates with polyethylene glycol
(inhibition of binding of integrin .alpha.4.beta.1 to VCAM-1 or fibronectin with fibronectin CS1 domain peptide analog inhibitors)

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     (FILE 'HOME' ENTERED AT 08:01:33 ON 10 JUN 2002)
               SET COST OFF

     FILE 'REGISTRY' ENTERED AT 08:01:43 ON 10 JUN 2002
               E EILDV/SQEP
L1           16 S E3
L2          512 S EILDV/SQSP
L3          496 S L2 NOT L1
               SAV L1 GAM251073A/A
               SAV L3 GAM251073B/A

     FILE 'HCAOLD' ENTERED AT 08:02:50 ON 10 JUN 2002
L4            0 S L1 OR L3

     FILE 'HCAPLUS' ENTERED AT 08:02:59 ON 10 JUN 2002
L5           20 S L1
L6          351 S L3
L7            9 S EILDV
               E LOBB R/AU
L8          113 S E3,E5,E7,E8
               E BURKLY L/AU
L9           82 S E3-E6
               E BIOGEN/PA,CS
L10         647 S E3-E56
L11           4 S L5-L7 AND L8-L10
L12         363 S L5-L7
L13           2 S L12 AND ?ASTHMA?
               E ASTHMA/CT
               E E3+ALL
L14        9231 S E2+NT
               E E4+ALL
L15        6156 S E6,E5+NT
               E E10+ALL
               E E5+ALL
L16        8875 S E5,E4+NT
               E E11+ALL
               E E6+ALL
L17         681 S E4,E3+NT
L18           1 S L12 AND L14-L17
L19          35 S L12 AND (LUNG OR PULMON? OR AIRWAY OR AIR WAY OR BRONCH? OR R
L20           2 S L13,L18
               E RESPIR/CT
               E E13+ALL
L21       38379 S E5,E4+NT
L22         944 S E36+NT
               E E38+ALL
L23      115430 S E4+NT
               E E3+AKK
               E E3+ALL
               E E73+ALL
L24         700 S E2
               E RESPIRATORY TRACT/CT
               E E42+ALL
L25         177 S E1
               E E2+ALL
L26      115430 S E4+NT
L27          18 S L12 AND L21-L26
L28          18 S L27 AND L19
L29          23 S L20,L28,L11
L30          16 S L19 NOT L29
L31           1 S L30 AND RESPIRATORY DISTRESS SYNDROME
L32          24 S L29,L31
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L33           3 S L12 AND HYPERSENSITIV?
L34           3 S L12 AND ?ALLERG?
L35           5 S L33,L34
L36           1 S L35 AND L32
L37           4 S L35 NOT L32
L38          24 S L32,L36
L39           5 S L38 AND (PY<=1993 OR PRY<=1993 OR AY<=1993)
L40           1 S L39 AND L13,L18
L41          19 S L38 NOT L39
                SEL DN 18
L42           1 S E1 AND L41
L43           2 S L40,L42
L44           4 S L11,L20 NOT L43
                SEL HIT RN L43

     FILE 'REGISTRY' ENTERED AT 08:23:14 ON 10 JUN 2002
L45           9 S E2-E10
L46           9 S L45 AND L1-L3

     FILE 'USPATFULL, USPAT2' ENTERED AT 08:23:49 ON 10 JUN 2002
L47          53 S L1,L3
L48          13 S L47 AND ?ASTHMA?
L49           1 S L47 AND (ASTHMA? OR ANTIASTHMA?)/CT
L50          13 S L48,L49
L51           0 S L50 AND (PY<=1993 OR PRY<=1993)
L52           4 S L47 AND (PY<=1993 OR PRY<=1993)
L53          27 S L47 AND (BRONCH? OR LUNG? OR PULMONARY? OR RESPIRATION? OR RE
L54           0 S L52 AND L53

     FILE 'HCAPLUS' ENTERED AT 08:26:10 ON 10 JUN 2002

     FILE 'REGISTRY' ENTERED AT 08:26:18 ON 10 JUN 2002

     FILE 'HCAPLUS' ENTERED AT 08:26:38 ON 10 JUN 2002
                SEL HIT RN L44

     FILE 'REGISTRY' ENTERED AT 08:27:17 ON 10 JUN 2002
L55           6 S E11-E16
L56           4 S L55 AND L1-L3 NOT L46

     FILE 'USPATFULL, USPAT2' ENTERED AT 08:27:50 ON 10 JUN 2002
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